



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 116579

TO: Rita Mitra  
Location: REM-3B65  
Art Unit: 1653  
Monday, March 15, 2004

Case Serial Number: 09/976740

From: Toby Port  
Location: Biotech-Chem Library  
Remsen 1A59  
Phone: 571-272-2523

toby.port@uspto.gov

### Search Notes

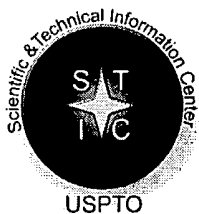
Dear Examiner Mitra,

Here are the results of your search.  
Please feel free to contact me if you have any questions.

Toby Port

*Look for WO ref.  
+ Pat. here.  
NPL ordered.*





# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 116472

TO: Rita Mitra  
Location: REM/3B65  
Art Unit: 1653  
Monday, March 15, 2004

Case Serial Number: 09/976740

From: Barb O'Bryen  
Location: Biotech-Chem Library  
Remsen E01A69  
Phone: 571-272-2518

barbara.obryen@uspto.gov

### Search Notes

# RUSH

~~Not elected~~  
7, 19, 20, 21, 22





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 20:46:42 ; Search time 37.6157 Seconds

(without alignments)  
2544.725 Million cell updates/sec

Title: US-09-976-740-20  
Perfect score: 136  
Sequence: 1 EREDDDEDEDEDDVEGSEVPESD 26

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=published.Applications.NA -QFM=faststep -SUFFIX=trmp -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blonsum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=2000000000 -USER=US09976740 @CGN 1.1 712 @runatc.10032004.094549.19586  
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-XGAPOP=6 -Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:\*

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5: /cgna2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
6: /cgna2\_6/ptodata/1/pubpna/PTCUS\_PUBCOMB.seq:\*  
7: /cgna2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
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9: /cgna2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgna2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
11: /cgna2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*  
12: /cgna2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
13: /cgna2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
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17: /cgna2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
18: /cgna2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Match Length	ID	Description
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1	136	100.0	78	9	US-09-962-055-31	Sequence 31, Appl
2	136	100.0	78	9	US-09-976-740-31	Sequence 31, Appl
3	136	100.0	78	12	US-10-671-242-31	Sequence 31, Appl
4	136	100.0	78	13	US-10-023-529-31	Sequence 31, Appl
5	136	100.0	78	13	US-10-023-529-31	Sequence 31, Appl
6	136	100.0	78	15	US-10-616-187-31	Sequence 31, Appl
7	136	100.0	1208	9	US-09-962-055-16	Sequence 16, Appl
8	136	100.0	1208	9	US-09-976-740-16	Sequence 16, Appl
9	136	100.0	1208	12	US-10-671-242-16	Sequence 16, Appl
10	136	100.0	1208	13	US-10-023-529-16	Sequence 16, Appl
11	136	100.0	1208	13	US-10-023-529-16	Sequence 16, Appl
12	136	100.0	1208	15	US-10-616-187-16	Sequence 16, Appl
13	136	100.0	1336	14	US-10-102-806-247	Sequence 247, App
14	136	100.0	1445	10	US-09-945-527-6	Sequence 6, Appl
15	136	100.0	1614	9	US-09-976-740-45	Sequence 45, Appl
16	136	100.0	1614	12	US-10-671-242-45	Sequence 45, Appl
17	136	100.0	1614	13	US-10-023-529-45	Sequence 45, Appl
18	136	100.0	1614	13	US-10-023-529-45	Sequence 45, Appl
19	136	100.0	1614	15	US-10-616-187-45	Sequence 45, Appl
20	136	100.0	12425	9	US-09-976-740-50	Sequence 50, Appl
21	136	100.0	12425	12	US-10-671-242-50	Sequence 50, Appl
22	136	100.0	12425	13	US-10-023-529-50	Sequence 50, Appl
23	136	100.0	12425	13	US-10-023-529-50	Sequence 50, Appl
24	136	100.0	12425	15	US-10-616-187-50	Sequence 50, Appl
25	104.5	76.8	84	9	US-09-962-055-37	Sequence 37, Appl
26	104.5	76.8	84	9	US-09-976-740-37	Sequence 37, Appl
27	104.5	76.8	84	12	US-10-671-242-37	Sequence 37, Appl
28	104.5	76.8	84	13	US-10-023-529-37	Sequence 37, Appl
29	104.5	76.8	84	13	US-10-023-529-37	Sequence 37, Appl
30	104.5	76.8	84	15	US-10-616-187-37	Sequence 37, Appl
31	104.5	76.8	1362	9	US-09-962-055-11	Sequence 11, Appl
32	104.5	76.8	1362	9	US-09-976-740-12	Sequence 12, Appl
33	104.5	76.8	1362	12	US-10-671-242-12	Sequence 12, Appl
34	104.5	76.8	1362	13	US-10-023-529-12	Sequence 12, Appl
35	104.5	76.8	1362	13	US-10-023-529-12	Sequence 12, Appl
36	104.5	76.8	1362	15	US-10-616-187-12	Sequence 12, Appl
37	104.5	76.8	1422	9	US-09-962-055-13	Sequence 13, Appl
38	104.5	76.8	1422	9	US-09-976-740-13	Sequence 13, Appl
39	104.5	76.8	1422	12	US-10-671-242-13	Sequence 13, Appl
40	104.5	76.8	1422	13	US-10-023-529-13	Sequence 13, Appl
41	104.5	76.8	1422	13	US-10-023-529-13	Sequence 13, Appl
42	104.5	76.8	1422	15	US-10-616-187-13	Sequence 13, Appl
43	104.5	76.8	1617	9	US-09-962-055-11	Sequence 11, Appl
44	104.5	76.8	1617	9	US-09-976-740-11	Sequence 11, Appl
45	104.5	76.8	1617	12	US-10-671-242-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-09-962-055-31  
Sequence 31, Application US/09962055  
Patent No. US20020052033A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS



	RESULT 4	
	US-10-023-529-31	
	/ Sequence 31, Application US/10023529	
	/ Publication No. US20020129385A1	
	GENERAL INFORMATION:	
	/ APPLICANT: Lees, Ann M.	
	/ APPLICANT: Lees, Robert S.	
	/ APPLICANT: Law, Simon W.	
	/ APPLICANT: Arjona, Anibal A.	
	TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATING	
	TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING	
	TITLE OF INVENTION: ATHEROSCLEROSIS	
	FILE REFERENCE: 10797-004001	
	CURRENT APPLICATION NUMBER: US/10/023,529	
	CURRENT FILING DATE: 2001-12-17	
	PRIOR APPLICATION NUMBER: 09/616,289	
	PRIOR FILING DATE: 2000-07-14	
	PRIOR APPLICATION NUMBER: US 09/517,849	
	PRIOR FILING DATE: 2000-03-02	
	PRIOR APPLICATION NUMBER: US 08/979,608	
	PRIOR FILING DATE: 1997-11-26	
	PRIOR APPLICATION NUMBER: US 60/031,930	
	PRIOR FILING DATE: 1996-11-27	
	PRIOR APPLICATION NUMBER: US 60/048,547	
	PRIOR FILING DATE: 1997-06-03	
	NUMBER OF SEQ ID NOS: 53	
	SOFTWARE: FastSeq for Windows Version 4.0	
	SEQ ID NO 31	
	LENGTH: 78	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-10-023-529-31	
	Alignment Scores:	
	Pred. No.: 1e-12 Length: 78	
	Score: 136.00 Matches: 26	
	Percent Similarity: 100.00% Conservative: 0	
	Best Local Similarity: 100.00% Mismatches: 0	
	Query Match: 100.00% Indels: 0	
	DB: Gaps: 0	
	US-09-976-740-20 (1-26) x US-10-023-529-31 (1-78)	
QY	1 GluGluGluGluAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 20	
Db	1 GAAGGGAGAAGATGATGATGAAGATGAAGATGAAGATGAAGATGTCTCAGAGGCTCT 60	
QY	21 GluValProGluSerAsp 26	
Db	61 GAAGTCCCGAGAGTGAC 78	
	RESULT 5	
	US-10-023-523-31	
	/ Sequence 31, Application US/10023523	
	/ Publication No. US20020152485A1	
	GENERAL INFORMATION:	
	/ APPLICANT: Lees, Ann M.	
	/ APPLICANT: Lees, Robert S.	
	/ APPLICANT: Law, Simon W.	
	/ APPLICANT: Arjona, Anibal A.	
	TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING	
	TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING	
	TITLE OF INVENTION: ATHEROSCLEROSIS	
	FILE REFERENCE: 10797-004001	
	CURRENT APPLICATION NUMBER: US/10/023,523	
	CURRENT FILING DATE: 2001-12-17	
	PRIOR APPLICATION NUMBER: US/09/616,289	
	PRIOR FILING DATE: 2000-07-14	
	PRIOR APPLICATION NUMBER: US 09/517,849	
	PRIOR FILING DATE: 2000-03-02	
	PRIOR APPLICATION NUMBER: US 08/979,608	
	PRIOR FILING DATE: 1997-11-26	
	PRIOR APPLICATION NUMBER: US 60/031,930	
	PRIOR FILING DATE: 1997-06-03	
	NUMBER OF SEQ ID NOS: 53	
	SOFTWARE: FastSeq for Windows Version 4.0	
	SEQ ID NO 31	
	LENGTH: 78	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-10-616-187-31	
	Alignment Scores:	
	Pred. No.: 1e-12 Length: 78	
	Score: 136.00 Matches: 26	
	Percent Similarity: 100.00% Conservative: 0	
	Best Local Similarity: 100.00% Mismatches: 0	
	Query Match: 100.00% Indels: 0	
	DB: Gaps: 0	
	US-09-976-740-20 (1-26) x US-10-616-187-31 (1-78)	
QY	1 GluGluGluGluAspAspGluAspGluAspGluGluGluAspAspValSerGluGlySer 20	
Db	1 GAAGAGAAAGATGATGATGAAGATGAAGATGAAGATGAAGATGTCTCAGAGGCTCT 60	
QY	21 GluValProGluSerAsp 26	
Db	61 GAAGTCCCGAGAGTGAC 78	
	RESULT 6	
	US-10-616-187-31	
	/ Sequence 31, Application US/10616187	
	/ Publication No. US20040013668A1	
	GENERAL INFORMATION:	
	/ APPLICANT: Lees, Ann M.	
	/ APPLICANT: Lees, Robert S.	
	/ APPLICANT: Law, Simon W.	
	/ APPLICANT: Arjona, Anibal A.	
	TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING	
	TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING	
	TITLE OF INVENTION: ATHEROSCLEROSIS	
	FILE REFERENCE: 10797-004001	
	CURRENT APPLICATION NUMBER: US/10/616,187	
	CURRENT FILING DATE: 2003-07-09	
	PRIOR APPLICATION NUMBER: US/09/616,289	
	PRIOR FILING DATE: 2000-07-14	
	PRIOR APPLICATION NUMBER: US 09/517,849	
	PRIOR FILING DATE: 2000-03-02	
	PRIOR APPLICATION NUMBER: US 08/979,608	
	PRIOR FILING DATE: 1997-11-26	
	PRIOR APPLICATION NUMBER: US 60/031,930	
	PRIOR FILING DATE: 1996-11-27	
	PRIOR APPLICATION NUMBER: US 60/048,547	
	PRIOR FILING DATE: 1997-06-03	
	NUMBER OF SEQ ID NOS: 53	
	SOFTWARE: FastSeq for Windows Version 4.0	
	SEQ ID NO 31	
	LENGTH: 78	
	TYPE: DNA	
	ORGANISM: Homo sapiens	
	US-10-616-187-31	
	Alignment Scores:	
	Pred. No.: 1e-12 Length: 78	
	Score: 136.00 Matches: 26	
	Percent Similarity: 100.00% Conservative: 0	
	Best Local Similarity: 100.00% Mismatches: 0	
	Query Match: 100.00% Indels: 0	
	DB: Gaps: 0	
	US-09-976-740-20 (1-26) x US-10-616-187-31 (1-78)	
QY	1 GluGluGluGluAspAspGluAspGluAspGluGluGluAspAspValSerGluGlySer 20	
Db	1 GAAGAGAAAGATGATGATGAAGATGAAGATGAAGATGAAGATGTCTCAGAGGCTCT 60	



PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-10-671-242-16

Alignment Scores:  
Pred. No.: 1,52e-11 Length: 1208  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-976-740-20 (1-26) x US-10-671-242-16 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPSPGIUAASPGIUAASPGIUAASPVAlserGIUGIYser 20  
DB 22 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAAGATGATGATCAAGAGGCTCT 81

QY 21 GIUValProGIUserASP 26  
DB 82 GAAGTGCCCGAGAGTGAC 99

RESULT 10  
US-10-023-529-16  
Sequence 16, Application US/10023529  
Publication No. US20020129388A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-10-023-529-16

Alignment Scores:  
Pred. No.: 1,52e-11 Length: 1208  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-976-740-20 (1-26) x US-10-023-529-16 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPSPGIUAASPGIUAASPGIUAASPVAlserGIUGIYser 20  
DB 22 GAAGAGGAGAGATGATGATGAAGATGAAGATGAAGATGAAGATGATGATCAAGAGGCTCT 81

QY 21 GIUValProGIUserASP 26  
DB 82 GAAGTGCCCGAGAGTGAC 99

RESULT 11  
US-10-023-523-16  
Sequence 16, Application US/10023523  
Publication No. US20020152485A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,523  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-10-023-523-16

Alignment Scores:  
Pred. No.: 1,52e-11 Length: 1208  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-976-740-20 (1-26) x US-10-023-523-16 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPSPGIUAASPGIUAASPGIUAASPVAlserGIUGIYser 20  
DB 22 GAAGAGGAGAGATGATGATGAAGATGAAGATGAAGATGAAGATGATGATCAAGAGGCTCT 81

QY 21 GIUValProGIUserASP 26  
DB 82 GAAGTGCCCGAGAGTGAC 99

RESULT 12

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US-10-616-187-16
; Sequence 16, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon M.
; APPLICANT: Atjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-616-187-16

Alignment Scores:
Pred. No.: 1,52e-11 Length: 1208
Score: 136.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-976-740-20 (1-26) x US-10-616-187-16 (1-1208)
QY 1 GUGUGUGUGUASPAPAPGUAAPGUAAPGUGUGUASPAPVAlSerGIUGlySer 20
Db 22 GAAGAGAGAGAGATGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 81
QY 21 GluValProGluSerASP 26
Db 82 GAAGTGGCCGAGAGTGAC 99

RESULT 13
US-10-102-806-247
; Sequence 247, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103Plc1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 247
; LENGTH: 1336
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (1336)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-247

Alignment Scores:
Pred. No.: 1,68e-11 Length: 1336
Score: 136.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-976-740-20 (1-26) x US-10-102-806-247 (1-1336)
QY 1 GUGUGUGUGUASPAPAPGUAAPGUAAPGUGUGUASPAPVAlSerGIUGlySer 20
Db 94 GAAGAGAGAGAGATGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 153
QY 21 GluValProGluSerASP 26
Db 154 GAAGTGGCCGAGAGTGAC 171

RESULT 14
US-09-945-527-6
; Sequence 6, Application US/09945527
; Publication No. US2003005588A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US2003005588A1 Nucleic Acid Molecules Encoding
; FILE REFERENCE: 35800/237985
; CURRENT APPLICATION NUMBER: US/09/945,527
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-945-527-6

Alignment Scores:
Pred. No.: 1,82e-11 Length: 1445
Score: 136.00 Matches: 26
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-976-740-20 (1-26) x US-09-945-527-6 (1-1445)
QY 1 GUGUGUGUGUASPAPAPGUAAPGUAAPGUGUGUASPAPVAlSerGIUGlySer 20
Db 207 GAAGAGAGAGAGATGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 266
QY 21 GluValProGluSerASP 26
Db 267 GAAGTGGCCGAGAGTGAC 284

RESULT 15
US-09-976-740-45
; Sequence 45, Application US/09976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
```

```

APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/766,740
CURRENT FILING DATE: 2001-10-12
PRIORITY APPLICATION NUMBER: 09/616,289
PRIORITY FILING DATE: 2000-07-14
PRIORITY APPLICATION NUMBER: US 08/979,608
PRIORITY FILING DATE: 1997-11-26
PRIORITY APPLICATION NUMBER: US 60/031,930
PRIORITY FILING DATE: 1996-11-27
PRIORITY APPLICATION NUMBER: US 60/048,547
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1614)
US-09-976-740-45

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Alignment Scores:	
Pred. No.:	2,036-11
Score:	136.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	1614
Matches:	26
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-976-740-20 (1-26) X US-09-976-740-45 (1-1614)

<i>Qy</i>	1	GluGluGluGluGluAspAspSerGluAspGluAspGluGluAspValSerCysGlySer	20
D <sub>b</sub>	985	GAAGACGAAGAAGATCATGCATGAATCAATCAAGTGTCTCGAAGGGCTCT	1044
<i>Qy</i>	21	GluValProGluSerAsp	26
D <sub>b</sub>	1045	GAAGTCGCCGAGAGTGAC	1062

Search completed: March 13, 2004, 04:26:14  
Job time : 38.6157 secs









REFERENCE 1 (bases 1 to 275)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 CGNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CGNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
 Insert length: 1112 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 229.  
 Location/Qualifiers  
 1..275  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1351450"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /clone\_id="NCI CGAP GCBI1"  
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 15'-TGTTACCAATCTGAAGATGAGGCGCGCTCATTTTCTTTT-3'  
 1. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pRT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
1	136.00	275	26
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-20 (1-26) x AA806888 (1-275)

QY 1 GIUGIUGIUGIUAAPSPGIIUASPGLIUGIUAASPVALSergIUGIYser 20  
 |||||  
 DB 85 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGATGTCAGAGGGCTCT 144  
 |||||  
 QY 21 GIUVALProGIUserASP 26  
 |||||  
 DB 145 GAAGTGCCCGAGAGTGAC 162  
 |||||

RESULT 4  
 AA810871 278 bp mRNA linear EST 19-FEB-1998  
 LOCUS AA810871  
 DEFINITION o64605.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1336184 3'  
 similar to contains element PTR7 repetitive element ;, mRNA  
 sequence.  
 ACCESSION AA810871  
 VERSION AA810871.1 GI:2880482  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 278)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 CGNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CGNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
 Insert length: 1143 Std Error: 0.00  
 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 269.  
 Location/Qualifiers  
 1..278  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1336184"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /clone\_id="NCI CGAP GCBI1"  
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 15'-TGTTACCAATCTGAAGATGAGGCGCGCTCATTTTCTTTT-3'  
 1. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pRT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
1	136.00	278	26
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-20 (1-26) x AA810871 (1-278)

QY 1 GIUGIUGIUGIUAAPSPGIIUASPGLIUGIUAASPVALSergIUGIYser 20  
 |||||  
 DB 82 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGATGTCAGAGGGCTCT 141  
 |||||  
 QY 21 GIUVALProGIUserASP 26  
 |||||  
 DB 142 GAAGTGCCCGAGAGTGAC 159  
 |||||

RESULT 5  
 AA766034 284 bp mRNA linear EST 08-FEB-1998  
 LOCUS AA766034  
 DEFINITION ca15b09.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1305017 3'  
 similar to contains element MER22 repetitive element ;, mRNA  
 sequence.  
 ACCESSION AA766034  
 VERSION AA766034.1 GI:2817272  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 284)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/HLN at:  
[www.bio.ill.gov/birop/image/image.html](http://www.bio.ill.gov/birop/image/image.html)  
Insert Length: 1100 Std Error: 0.00  
Seq primer: -40ml3 fwd. RT from Amersham  
High quality sequence stop: 283.  
Location/Qualifiers  
1..284  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3643712"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP GCBI"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCATCTGAAGTGGAGCGCCGCTCATTTTCTTTTCTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ALIGNMENT SCORES:  
Pred. No.: 1.69e-07 Length: 284  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-20 (1-26) x AA766034 (1-284)

QY 1 GUGUGUGUGUASPAPSPGUASPGLUASPSPVAlSerGIUGlySer 20  
DB 81 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 140

QY 21 GUUAlProGIUGSerASP 26  
DB 141 GAAGTGGCCGAGAGTGC 158

RESULT 6  
BF194967  
LOCUS 302 bp mRNA linear EST 03-NOV-2000  
DEFINITION 709105.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:3643712 3'  
similar to contains element TARI TARI repetitive element ;, mRNA  
sequence.  
ACCESSION BF194967  
VERSION BF194967.1 GI:11081346  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 302)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento  
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/HLN, send email to:  
[info@image.ill.gov](mailto:info@image.ill.gov).  
Location/Qualifiers  
1..302  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3643712"  
/tissue\_type="fibrocyte"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NCI CGAP Ov18"  
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCATCTGAAGTGGAGCGCCGCTCATTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ALIGNMENT SCORES:  
Pred. No.: 1.82e-07 Length: 302  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-976-740-20 (1-26) x BF194967 (1-302)

QY 1 GUGUGUGUGUASPAPSPGUASPGLUASPSPVAlSerGIUGlySer 20  
DB 168 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 227

QY 21 GUUAlProGIUGSerASP 26  
DB 228 GAAGTGGCCGAGAGTGC 245

RESULT 7  
A1470106  
LOCUS 322 bp mRNA linear EST 14-APR-1999  
DEFINITION U90909.x1 Soares NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
IMAGE:2148832 3' similar to contains TARI.b2 P7b5 repetitive  
element ;, mRNA sequence.  
ACCESSION A1470106  
VERSION A1470106.1 GI:4332196  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index



Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
infoimage.llnl.gov

Seq primer: -400P from Gibco  
High quality sequence stop: 325.  
Location/Qualifiers

## FEATURES

## Source

1. 345  
/organism="Homo sapiens"  
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/lab\_host="DH10B (phage-resistant)"  
/note="Organ: ovary; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAACTGGAGGCGCCGCTCATTTTCTTTTCTTTT 3'];  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

## Alignment Scores:

Pred. No.:	2.12e-07	Length:	345
Score:	136.00	Matches:	26
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-976-740-20 (1-26) x BP941758 (1-345)

QY 1 GUGUGUGUGUASPAPSPGUAASPGLUASPAPSPALSERGLUGLYSER 20

DB 159 GAAGAGAGAGAGATATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 218

QY 21 GUUVALPROGUSERSASP 26

DB 219 GAAGTGGCCGAGAGTGAC 236

## RESULT 10

## LOCUS

AA769505 367 bp mRNA linear EST 07-FEB-1998

DEFINITION n235p01.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1289737 3', mRNA

sequence.

AA769505

AA769505.1 GI:2820743

EST.

Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 367)

REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)

Tissue Procurement: Louis M. Straud, M.D., Ph.D., David Allman,

Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Insert Length: 1136 Std Error: 0.00  
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High quality sequence stop: 366.  
Location/Qualifiers

## FEATURES

## Source

1. 367  
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/mol\_type="mRNA"  
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/clone="IMAGE:1289737"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GCBI"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Straud (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAACTGGAGGCGCCGCTCATTTTCTTTTCTTTT-3',  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

## Alignment Scores:

Pred. No.:	2.27e-07	Length:	367
Score:	136.00	Matches:	26
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-20 (1-26) x AA769505 (1-367)

QY 1 GUGUGUGUGUASPAPSPGUAASPGLUASPAPSPALSERGLUGLYSER 20

DB 105 GAAGAGAGAGAGATATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 164

QY 21 GUUVALPROGUSERSASP 26

DB 165 GAAGTGGCCGAGAGTGAC 182

## RESULT 11

## LOCUS

AM845391 383 bp mRNA linear EST 19-MAY-2000

DEFINITION CM4-CT0045-180200-512-h05 CT0045 Homo sapiens cDNA, mRNA sequence.

AM845391

AM845391.1 GI:7940908

EST.

Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

1 (bases 1 to 383)

REFERENCE Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsushima, A., Bata, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, U.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

CONTACT: Simpson A.J.C.

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil



image:11n1.gov/image/html/iresources.shtml  
Possible reversed clone: polyT not found  
Seq primer: -40UP from Gibco  
High quality sequence stop: 397.  
Location/Qualifiers  
1..397

FEATURES  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2950790"  
/cissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_1ib="NCI CGAP GC6"  
/note="Vector: p7713D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI-CGAP-GC4 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
Pred. No.: 2,49e-07 Length: 397  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-976-740-20 (1-26) x AW594381 (1-397)

QY 1 GUGUGUGUGUASPAPSPGUAAPGUAAPGUGUASPAPYALSERGIUGLYSER 20  
DB 177 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 236  
QY 21 GUUVALPROGLUSERASP 26  
DB 237 GAAGTCCCGAGAGTGAC 254

RESULT 14  
AM134620 412 bp mRNA linear EST 28-OCT-1998  
LOCUS  
DEFINITION  
IMAGE:2712710 3', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
1..412  
Location/Qualifiers

## ORIGIN

Alignment Scores:  
Pred. No.: 2,59e-07 Length: 412  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0  
US-09-976-740-20 (1-26) x AM134620 (1-412)

QY 1 GUUGUGUGUGUASPAPSPGUAAPGUAAPGUGUASPAPYALSERGIUGLYSER 20  
DB 176 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 235  
QY 21 GUUVALPROGLUSERASP 26  
DB 236 GAAGTCCCGAGAGTGAC 253

RESULT 15  
A1097526 429 bp mRNA linear EST 26-OCT-1998  
LOCUS  
DEFINITION  
IMAGE:1707118 3' similar to contains TAR1.b2 PTRS repetitive element /, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens







GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:49:56 ; Search time 167.073 Seconds

(without alignments)  
2853.675 Million cell updates/sec

Title: US-09-976-740-21  
Perfect score: 54  
Sequence: 1 VSEGEVPESD 11

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-DB=genemb1 -GWT=fastap -SUFFIX=ise -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFM=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-DEV\_TIMECUT=120 -WARN\_TIMECUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmb1.\*  
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2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
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7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vt:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_ov:\*  
22: em\_or:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vi:\*  
30: em\_hcg\_hum:\*  
31: em\_hcg\_inv:\*  
32: em\_hcg\_other:\*  
33: em\_hcg\_mus:\*  
34: em\_hcg\_pln:\*  
35: em\_hcg\_rod:\*  
36: em\_hcg\_mam:\*  
37: em\_hcg\_vrt:\*  
38: em\_sy:\*  
39: em\_hcgo\_hum:\*  
40: em\_hcgo\_mus:\*  
41: em\_hcgo\_other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	54	100.0	33	6	AR199540 Sequence
2	54	100.0	33	6	AR374692 Sequence
3	54	100.0	33	6	AR409327 Sequence
4	54	100.0	33	6	AX239589 Sequence
5	54	100.0	33	6	BD056454 Novel Low
6	54	100.0	36	6	AR199546 Sequence
7	54	100.0	36	6	AR374698 Sequence
8	54	100.0	36	6	AR409333 Sequence
9	54	100.0	36	6	AX239595 Sequence
10	54	100.0	36	6	BD056460 Novel Low
11	54	100.0	78	6	AR199539 Sequence
12	54	100.0	78	6	AR374691 Sequence
13	54	100.0	78	6	AR409326 Sequence
14	54	100.0	78	6	AX239588 Sequence
15	54	100.0	78	6	BD056453 Novel Low
16	54	100.0	84	6	AR199545 Sequence
17	54	100.0	84	6	AR374697 Sequence
18	54	100.0	84	6	AR409332 Sequence
19	54	100.0	84	6	AX239594 Sequence
20	54	100.0	84	6	BD056459 Novel Low
21	54	100.0	982	9	BC007384 Homo sapi
22	54	100.0	1208	6	AR199535 Sequence
23	54	100.0	1208	6	AR374687 Sequence
24	54	100.0	1208	6	AR409322 Sequence
25	54	100.0	1208	6	AX239573 Sequence
26	54	100.0	1208	6	BD056449 Novel Low
27	54	100.0	1362	6	AR199531 Sequence
28	54	100.0	1362	6	AR374683 Sequence
29	54	100.0	1362	6	AR409318 Sequence
30	54	100.0	1362	6	AX239569 Sequence
31	54	100.0	1362	6	BD056445 Novel Low
32	54	100.0	1422	6	AR199532 Sequence
33	54	100.0	1422	6	AR374684 Sequence
34	54	100.0	1422	6	AR409319 Sequence
35	54	100.0	1422	6	AX239570 Sequence
36	54	100.0	1422	6	BD056446 Novel Low
37	54	100.0	1470	6	BC030129 Homo sapi
38	54	100.0	1614	6	AR409337 Sequence
39	54	100.0	1614	6	AX239602 Sequence
40	54	100.0	1617	6	AR199530 Sequence
41	54	100.0	1617	6	AR374682 Sequence
42	54	100.0	1617	6	AR409317 Sequence
43	54	100.0	1617	6	AX239568 Sequence
44	54	100.0	1617	6	BD056444 Novel Low
45	54	100.0	1617	9	AY453840 Homo sapi

## ALIGNMENTS

RESULT 1

AR199540  
LOCUS AR199540 33 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 32 from patent US 6355451.  
ACCESSION AR199540  
VERSION AR199540.1 GI:20249614  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 32 12-MAR-2002;  
FEATURES  
source  
1..33  
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ORIGIN  
Alignment Scores:  
Pred. No.: 0.00285 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-21 (1-11) x AR199540 (1-33)

QY 1 ValSerGIuGIySerGIuValProGIuSerAsp 11  
DB 1 GTGTCAAGAGGGCTCTGAAGTGCCTCGAGAGTGC 33

RESULT 2  
LOCUS AR374692 33 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 32 from patent US 6605588.  
ACCESSION AR374692  
VERSION AR374692.1 GI:40077507  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 32 12-AUG-2003;  
FEATURES  
source  
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Alignment Scores:  
Pred. No.: 0.00285 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-21 (1-11) x AR374692 (1-33)

QY 1 ValSerGIuGIySerGIuValProGIuSerAsp 11  
DB 1 GTGTCAAGAGGGCTCTGAAGTGCCTCGAGAGTGC 33

RESULT 3  
LOCUS AR409327 33 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 32 from patent US 6632923.

ACCESSION AR409327  
VERSION AR409327.1 GI:40160115  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 32 14-OCT-2003;  
FEATURES  
source  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.00285 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-21 (1-11) x AR409327 (1-33)

QY 1 ValSerGIuGIySerGIuValProGIuSerAsp 11  
DB 1 GTGTCAAGAGGGCTCTGAAGTGCCTCGAGAGTGC 33

RESULT 4  
LOCUS AX239589 33 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 32 from Patent WO0164874.  
ACCESSION AX239589  
VERSION AX239589.1 GI:15797265  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in diagnosing  
and treating atherosclerosis  
JOURNAL Patent: WO 0164874-A 32 07-SEP-2001;  
FEATURES  
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ORIGIN  
Alignment Scores:  
Pred. No.: 0.00285 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-21 (1-11) x AX239589 (1-33)

QY 1 ValSerGIuGIySerGIuValProGIuSerAsp 11  
DB 1 GTGTCAAGAGGGCTCTGAAGTGCCTCGAGAGTGC 33

RESULT 5  
LOCUS BD056454 33 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel low density lipoprotein binding proteins and their use in

diagnosing and treating atherosclerosis.

ACCESSION BD056454  
VERSION BD056454.1 GI:22602060  
KEYWORDS JP 2001506983-A/12.  
SOURCE Aequorea victoria  
ORGANISM Aequorea victoria  
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae; Aequoreidae; Aequorea.

REFERENCE 1 (bases 1 to 33)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Novel low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: JP 2001506983-A 12 29-MAY-2001;  
BOSTON HEART FOUNDATION INC  
PN JP 2001506983-A/12  
PD 29-MAY-2001  
PR 26-NOV-1997 JP 1998524870  
PR 27-NOV-1996 US 60/031930.03-JUN-1997 US 60/048547 P1  
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC  
C07H21/00,  
PC C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/566 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key Location/Qualifiers.

FEATURES  
source 1..33  
/organism="Aequorea victoria"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:6100"

ORIGIN

Alignment Scores:  
Pred. No.: 0.00285 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-21 (1-11) x BD056454 (1-33)

QY 1 ValSerGluGlySerGluValProGluSerasp 11  
Db 1 GTGTCCAGAGGCGCTCGAGTGCCCGAGAGGTGAC 33

RESULT 6  
AR199546  
LOCUS AR199546  
DEFINITION Sequence 38 from patent US 6355451.  
ACCESSION AR199546  
VERSION AR199546.1 GI:20249620  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 36)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 38 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..36  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 0.00311 Length: 36  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

DB: 6 Gaps: 0

US-09-976-740-21 (1-11) x AR199546 (1-36)

QY 1 ValSerGluGlySerGluValProGluSerasp 11  
Db 4 GTGTCCAGAGGCGCTCGAGGTGCCCGAGAGCGAT 36

RESULT 7  
AR374698  
LOCUS AR374698  
DEFINITION Sequence 38 from patent US 6605588.  
ACCESSION AR374698  
VERSION AR374698.1 GI:40077513  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 36)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 38 12-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..36  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 0.00311 Length: 36  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-21 (1-11) x AR374698 (1-36)

QY 1 ValSerGluGlySerGluValProGluSerasp 11  
Db 4 GTGTCCAGAGGCGCTCGAGGTGCCCGAGAGCGAT 36

RESULT 8  
AR409333  
LOCUS AR409333  
DEFINITION Sequence 38 from patent US 6632923.  
ACCESSION AR409333  
VERSION AR409333.1 GI:40160121  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 36)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 38 14-OCT-2003;  
FEATURES Location/Qualifiers  
source 1..36  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Alignment Scores:  
Pred. No.: 0.00311 Length: 36  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
 DB 4 GTGTCCGAGGGCTCGAGGTGCGCCGAGAGCGCAT 36

RESULT 9  
 AX239595 36 bp DNA linear PAT 26-SEP-2001  
 LOCUS Sequence 38 from Patent WO0164874.  
 DEFINITION AX239595  
 ACCESSION AX239595  
 VERSION AX239595.1 GI:15797271  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis  
 Patent: WO 0164874-A 38 07-SEP-2001;  
 Boston Heart Foundation, Inc. (US)

JOURNAL  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"

FEATURES  
 source

ORIGIN

Alignment Scores:  
 Pred. No.: 0.00311 Length: 36  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-21 (1-11) x AX239595 (1-36)

QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
 DB 4 GTGTCCGAGGGCTCGAGGTGCGCCGAGAGCGCAT 36

RESULT 10  
 BD056460 36 bp DNA linear PAT 27-AUG-2002  
 LOCUS Novel low density lipoprotein binding proteins and their use in  
 DEFINITION diagnosing and treating atherosclerosis.  
 ACCESSION BD056460  
 VERSION BD056460.1 GI:22602066  
 KEYWORDS UP 2001506983-A/18.  
 SOURCE Aequorea victoria  
 ORGANISM Aequorea victoria  
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;  
 Aequoreidae; Aequorea.  
 1 (bases 1 to 36)

REFERENCE 1  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Novel low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis  
 Patent: JP 2001506983-A 18 29-MAY-2001;  
 BOSTON HEART FOUNDATION INC

JOURNAL  
 PN JP 2001506983-A/18  
 PD 29-MAY-2001  
 PR 26-NOV-1997 JP 1998524870  
 ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
 A61K38/04, A61K39/17, A61K39/00, A61K48/00, A61K51/08, PC  
 C07H21/00,  
 PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers

FEATURES  
 Location/Qualifiers

source 1..36  
 /organism="Aequorea victoria"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:6100"

ORIGIN

Alignment Scores:  
 Pred. No.: 0.00311 Length: 36  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-21 (1-11) x BD056460 (1-36)

QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
 DB 4 GTGTCCGAGGGCTCGAGGTGCGCCGAGAGCGCAT 36

RESULT 11  
 AR199539 78 bp DNA linear PAT 20-APR-2002  
 LOCUS Sequence 31 from patent US 6355451.  
 DEFINITION AR199539  
 ACCESSION AR199539  
 VERSION AR199539.1 GI:20249613  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 78)

REFERENCE 1  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis  
 Patent: US 6355451-A 31 12-MAR-2002;  
 Location/Qualifiers  
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 /organism="unknown"  
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ORIGIN

Alignment Scores:  
 Pred. No.: 0.00694 Length: 78  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-21 (1-11) x AR199539 (1-78)

QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
 DB 4 GTGTCCGAGGGCTCGAGGTGCGCCGAGAGCGCAT 78

RESULT 12  
 AR374691 78 bp DNA linear PAT 18-DEC-2003  
 LOCUS Sequence 31 from patent US 6605588.  
 DEFINITION AR374691  
 ACCESSION AR374691  
 VERSION AR374691.1 GI:40077506  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 78)

REFERENCE 1  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis  
 Patent: US 6605588-A 31 12-AUG-2003;  
 Location/Qualifiers  
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 /organism="unknown"

JOURNAL  
 source

FEATURES  
 source

ORIGIN /mol\_type="genomic DNA"

## Alignment Scores:

Pred. No.: 0.00694 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-21 (1-11) x AR374691 (1-78)

Cy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 46 GTGTCAGAGGGCTCTGAAGTCCCGAGAGTGAC 78

## RESULT 13

LOCUS AR409326 78 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 31 from patent US 6632923.  
ACCESSION AR409326  
VERSION AR409326.1 GI:40160114  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 78)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
JOURNAL diagnosing and treating atherosclerosis  
FEATURES location/Qualifiers  
source 1..78  
/organism="Unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00694 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-21 (1-11) x AR409326 (1-78)

Cy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 46 GTGTCAGAGGGCTCTGAAGTCCCGAGAGTGAC 78

## RESULT 14

LOCUS AX239588 78 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 31 from Patent WO0164874.  
ACCESSION AX239588  
VERSION AX239588.1 GI:15797264  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 78)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in diagnosing  
JOURNAL and treating atherosclerosis  
FEATURES Patent: WO 0164874-A 31 07-SEP-2001;  
source Boston Heart Foundation, Inc. (US)  
location/Qualifiers  
1..78  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

ORIGIN /db\_xref="taxon:9606"

## Alignment Scores:

Pred. No.: 0.00694 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-21 (1-11) x AX239588 (1-78)

Cy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 46 GTGTCAGAGGGCTCTGAAGTCCCGAGAGTGAC 78

## RESULT 15

LOCUS BD056453 78 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis.  
ACCESSION BD056453  
VERSION BD056453.1 GI:22602059  
KEYWORDS JP 2001506983-A/11.  
SOURCE Aequorea victoria  
ORGANISM Aequorea victoria  
REFERENCE 1 (bases 1 to 78)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Novel low density lipoprotein binding proteins and their use in  
JOURNAL diagnosing and treating atherosclerosis  
FEATURES Patent: JP 2001506983-A 11 29-MAY-2001;  
source BOSTON HEART FOUNDATION INC  
EN JP 2001506983-A/11  
PD 29-MAY-2001  
PF 26-NOV-1997 JP 1998524870  
PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI  
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC  
C07H21/00  
PC C07K7/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/68,G01N33/56 CC  
Strandedness: Single;  
CC Topology: Linear;  
FH Key location/Qualifiers  
source 1..78  
/organism="Aequorea victoria"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:6100"

## ORIGIN

## Alignment Scores:

Pred. No.: 0.00694 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-21 (1-11) x BD056453 (1-78)

Cy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 46 GTGTCAGAGGGCTCTGAAGTCCCGAGAGTGAC 78

Search completed: March 13, 2004, 00:35:26  
Job time : 167.073 secs





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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:48:14 ; Search time 17.4357 Seconds

(without alignments)  
2680.137 Million cell updates/sec

Title: US-09-976-740-21

Perfect score: 54

Sequence: 1 VSEGEVPEESD 11

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3173863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=N Geneseg.29Jan04 -CPMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloms62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MTLEN=0 -MAXLEN=200000000  
-USER=US09976740.@CGN\_1.1.1596.@runat.10032004.094547.19532 -NCPU=6 -ICPU=3  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N\_Geneseg.29Jan04:\*  
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2: geneseg1990s:\*  
3: geneseg2000s:\*  
4: geneseg2001as:\*  
5: geneseg2001bs:\*  
6: geneseg2002s:\*  
7: geneseg2003as:\*  
8: geneseg2003bs:\*  
9: geneseg2003cs:\*  
10: geneseg2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	33	5	Aah26504
2	54	100.0	36	5	Aah26510
3	54	100.0	78	5	Aah26503
4	54	100.0	84	5	Aah26509
5	54	100.0	1208	2	Aav32838
6	54	100.0	1208	5	Aah26494
7	54	100.0	1336	3	Aaf21860
8	54	100.0	1362	5	Aah26489

9	54	100.0	1422	5	Aah26490	Aah26490 Rabbit 10
10	54	100.0	1614	5	Aah26499	Aah26499 Human 10w
11	54	100.0	1617	2	Aav32835	Aav32835 Rabbit 10
12	54	100.0	1617	5	Aah26488	Aah26488 Rabbit 10
13	54	100.0	2561	5	Aah26500	Aah26500 Rabbit 10
14	54	100.0	12425	5	Aah26495	Aah26495 Human 10w
15	41	75.9	378	5	Aah26487	Aah26487 Novel hum
16	41	75.9	2512	9	ADC27704	ADC27704 Human col
17	40	74.1	374	3	AAI6147	AAI6147 Human sec
18	40	74.1	2428	9	ADB63004	ADB63004 Human CDN
19	40	74.1	3166	7	ABR42108	ABR42108 Toxicity-
20	40	74.1	3166	9	ADB58482	ADB58482 Toxicity-
21	40	74.1	3166	9	ADB53074	ADB53074 Primary r
22	39	72.2	1245	4	AA523121	AA523121 DNA encod
23	39	72.2	6728	3	AA35248	AA35248 Human BNP
24	39	72.2	11446	4	AAK90464	AAK90464 Human dig
25	39	72.2	14759	6	AA45087	AA45087 Human bon
26	39	72.2	14759	6	AA35955	AA35955 Human bon
27	39	72.2	160771	6	AB088179	AB088179 Human ost
28	38	70.4	405	8	ADA48469	ADA48469 Rice gene
29	38	70.4	411	3	AA69711	AA69711 Human ova
30	38	70.4	411	6	ABN72605	ABN72605 Ovarian c
31	38	70.4	411	8	ADA08770	ADA08770 Human ova
32	38	70.4	414	3	AAA69763	AAA69763 Human ova
33	38	70.4	414	6	ABN72657	ABN72657 Ovarian c
34	38	70.4	414	8	ADA08822	ADA08822 Human ova
35	38	70.4	447	7	ABZ52977	ABZ52977 Aspergill
36	38	70.4	471	3	AAH30503	AAH30503 Human col
37	38	70.4	495	8	ACH14529	ACH14529 Human adu
38	38	70.4	672	2	AA277478	AA277478 Human ova
39	38	70.4	782	3	AAH31119	AAH31119 Human col
40	38	70.4	1178	3	AA096936	AA096936 Human sec
41	38	70.4	1178	7	ABZ67115	ABZ67115 Human sec
42	38	70.4	1178	7	ABZ73508	ABZ73508 Secreted
43	38	70.4	1181	7	ABZ67870	ABZ67870 Human sec
44	38	70.4	1181	7	ABZ74310	ABZ74310 Secreted
45	38	70.4	1618	9	ADB53270	ADB53270 Primary r

#### ALIGNMENTS

RESULT 1

AAH26504  
AAH26504 standard; DNA; 33 BP.

AC	AAH26504;	
AC		
DT	12-NOV-2001 (first entry)	
XX		
DE	Low density lipoprotein binding protein (LBP) polynucleotide.	
XX		
KM	Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;	
XX	antiarteriosclerotic; therapy; diagnosis; vaccine, ss.	
OS	Mammalia.	
XX		
PN	WO200164874-A2.	
XX		
PD	07-SEP-2001.	
XX		
PF	28-FEB-2001; 2001WO-US006356.	
XX		
PR	02-MAR-2000; 2000US-00517849.	
XX		
PA	14-JUL-2000; 2000US-00616289.	
XX		
PA	(BOST-) BOSTON HEART FOUND INC.	
XX		
PI	Lees AM, Lees RS, Law SW, Arjona AA;	
XX		
DR	WPI; 2001-565505/63.	
XX		
PT	New isolated low density lipoprotein binding polypeptide for treating,	
PT	diagnosing and/or identifying therapeutic agents for atherosclerosis.	

XX PS Disclosure, Page 9, 143pp; English.

XX CC The present sequence is that of a polynucleotide encoding a fragment of

CC novel low density lipoprotein binding proteins (LBPs) of the invention

CC (see AAB82797-820). LBPs are capable of binding to native and methylated

CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel

CC LBPs and their fragments are claimed, as well as expression vectors,

CC cells and methods of producing the LBPs. Methods for determining if an

CC animal is at risk for atherosclerosis, and methods for evaluating an agent

CC for use in treating atherosclerosis, and methods for treating a cell

CC having an abnormality in structure or metabolism of LBP are also claimed,

CC as are pharmaceutical compositions comprising an LBP polypeptide or

CC nucleic acid, and vaccine compositions

XX SQ Sequence 33 BP; 7 A; 7 C; 13 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 54.00	33	11
Percent Similarity: 100.00%	Conservative: 0	
Best Local Similarity: 100.00%	Mismatches: 0	
Query Match: 100.00%	Indels: 0	
DB: 5	Gaps: 0	

US-09-976-740-21 (1-11) x AAH26504 (1-33)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11

Db 1 GTGTCCAGAGGCTCTGAGTCCCGAGAGTAC 33

RESULT 2

AAH26510

ID AAH26510 standard; DNA, 36 BP.

XX AC AAH26510;

XX DT 12-NOV-2001 (first entry)

XX DE Low density lipoprotein binding protein (LBP) polynucleotide.

XX KM Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;

XX KM antiarteriosclerotic; therapy; diagnosis; vaccine; ss.

XX OS Mammalia.

XX PN WO200164874-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006356.

XX PR 02-MAR-2000; 2000US-00517849.

XX PR 14-JUL-2000; 2000US-00616289.

XX PA (BOST-) BOSTON HEART FOUND INC.

XX PI Lees AM, Lees RS, Law SW, Arjona AA;

XX DR WPI; 2001-565505/63.

XX PT New isolated low density lipoprotein binding polypeptide for treating,

XX PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX PS Disclosure, Page 10; 143pp; English.

XX CC The present sequence is that of a polynucleotide encoding a fragment of

CC novel low density lipoprotein binding proteins (LBPs) of the invention

CC (see AAB82797-820). LBPs are capable of binding to native and methylated

CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel

CC LBPs and their fragments are claimed, as well as expression vectors,

CC cells and methods of producing the LBPs. Methods of determining if an

CC animal is at risk for atherosclerosis, methods for evaluating an agent

CC for use in treating atherosclerosis, and methods for treating a cell

CC having an abnormality in structure or metabolism of LBP are also claimed,

CC as are pharmaceutical compositions comprising an LBP polypeptide or

CC nucleic acid, and vaccine compositions

XX SQ Sequence 36 BP; 5 A; 9 C; 16 G; 6 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 54.00	36	11
Percent Similarity: 100.00%	Conservative: 0	
Best Local Similarity: 100.00%	Mismatches: 0	
Query Match: 100.00%	Indels: 0	
DB: 5	Gaps: 0	

US-09-976-740-21 (1-11) x AAH26510 (1-36)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11

Db 4 GTGTCCAGAGGCTCTGAGTCCCGAGAGCGAT 36

RESULT 3

AAH26503

ID AAH26503 standard; DNA, 78 BP.

XX AC AAH26503;

XX DT 12-NOV-2001 (first entry)

XX DE Low density lipoprotein binding protein (LBP) polynucleotide.

XX KM Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;

XX KM antiarteriosclerotic; therapy; diagnosis; vaccine; ss.

XX OS Mammalia.

XX PN WO200164874-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006356.

XX PR 02-MAR-2000; 2000US-00517849.

XX PR 14-JUL-2000; 2000US-00616289.

XX PA (BOST-) BOSTON HEART FOUND INC.

XX PI Lees AM, Lees RS, Law SW, Arjona AA;

XX DR WPI; 2001-565505/63.

XX PT New isolated low density lipoprotein binding polypeptide for treating,

XX PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX PS Disclosure, Page 9; 143pp; English.

XX CC The present sequence is that of a polynucleotide encoding a fragment of

CC novel low density lipoprotein binding proteins (LBPs) of the invention

CC (see AAB82797-820). LBPs are capable of binding to native and methylated

CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel

CC LBPs and their fragments are claimed, as well as expression vectors,

CC cells and methods of producing the LBPs. Methods of determining if an

CC animal is at risk for atherosclerosis, and methods for evaluating an agent

CC for use in treating atherosclerosis, and methods for treating a cell

CC having an abnormality in structure or metabolism of LBP are also claimed,

CC as are pharmaceutical compositions comprising an LBP polypeptide or

CC nucleic acid, and vaccine compositions

XX SQ Sequence 78 BP; 29 A; 7 C; 29 G; 13 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 54.00	78	11

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 5  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-09-976-740-21 (1-11) x AAH26503 (1-78)

QY 1 Valsergiuglysergiuvalprogluserasp 11  
DB 46 GTGTCCAGAGGCTCTGAGTGCCTCCGAGAGGAT 78

RESULT 4  
AAH26509  
ID AAH26509 standard; DNA, 84 BP.

AC AAH26509;

DT 12-NOV-2001 (first entry)

DB Low density lipoprotein binding protein (LBP) polynucleotide.

KM Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;  
KM antiarteriosclerotic; therapy; diagnosis; vaccine; ss.

OS Mammalia.

PN WO200164874-A2.

PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US006356.

PR 02-MAR-2000; 2000US-00517849.

PR 14-JUL-2000; 2000US-00616289.

PA (BOST-) BOSTON HEART POUND INC.

PI Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 2001-565505/63.

XX New isolated low density lipoprotein binding polypeptide for treating,  
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

PS Disclosure; Page 10; 143pp; English.

XX The present sequence is that of a polynucleotide encoding a fragment of  
CC novel low density lipoprotein binding proteins (LBPs) of the invention  
CC (see AAB8797-820). LBPs are capable of binding to native and methylated  
CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel  
CC LBPs and their fragments are claimed, as well as expression vectors,  
CC cells and methods of producing the LBPs. Methods of determining if an  
CC animal is at risk for atherosclerosis, methods for evaluating an agent  
CC for use in treating atherosclerosis, and methods for treating a cell  
CC having an abnormality in structure or metabolism of LBP are also claimed.  
CC as are pharmaceutical compositions comprising an LBP polypeptide or  
CC nucleic acid, and vaccine compositions

XX Sequence 84 BP; 22 A; 16 C; 40 G; 6 T; 0 U; 0 Other;

SO Alignment Scores:

Pred. No.: 0.0222 Length: 84  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-976-740-21 (1-11) x AAH26509 (1-84)

QY 1 Valsergiuglysergiuvalprogluserasp 11  
DB 52 GTGTCCAGAGGCTCTGAGTGCCTCCGAGAGGAT 84

RESULT 5  
AAV32838  
AAV32838 standard; cDNA; 1208 BP.

XX AAV32838;

XX 09-NOV-1998 (first entry)

XX Human low density lipoprotein binding protein LBP-2 cDNA.

KM Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;  
KM receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..654

FT misc\_feature 22..99

FT misc\_feature 22..66

FT misc\_feature 67..99

FT misc\_feature 622..651

FT misc\_feature 622..651

FT misc\_feature 622..651

PN WO9823282-A1.

PD 04-JUN-1998.

PF 26-NOV-1997; 97WO-US021857.

PR 27-NOV-1996; 96US-0031930P.

PR 03-JUN-1997; 97US-0048547P.

PA (BOST-) BOSTON HEART POUND INC.

PI Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 1998-322455/28.

XX P-PSDB; AAM49041.

XX Nucleic acid encoding low density lipoprotein binding proteins and  
PT related vectors - transformed cells, proteins, and modulators of binding,  
PT useful for treatment and diagnosis of atherosclerosis and for identifying  
PT subjects at risk.

PS Claim 9; Fig 16; 47pp; English.

XX This cDNA clone codes for novel human low density lipoprotein (LDL)  
CC binding protein LBP-2 (see AAM49041). It was isolated by screening human  
CC liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA  
CC clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAM49037-  
CC 42) are claimed. An abnormality in LBP metabolism or structure is  
CC diagnostic of a risk for atherosclerosis. The invention provides: methods  
CC for determining if an animal is at risk for atherosclerosis (e.g. for  
CC prenatal screening); methods for treating atherosclerosis (including gene  
CC therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent  
CC formation of atherosclerotic plaques; and methods for treating a cell  
CC having an abnormality in LBP structure or metabolism. Pharmaceutical and  
CC vaccine compositions are also provided, as well as recombinant vectors  
CC and host cells used to produce recombinant LBP

SO Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 0.463 Length: 1208

Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-09-976-740-21 (1-11) x AAV32838 (1-1208)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11

Db 67 GTGTCAAGAGGCTCTGTAAGTGCCTCGAGAGTGAC 99

RESULT 6

AAH26494

ID AAH26494 standard; cDNA; 1208 BP.

AC AAH26494;

DT 12-NOV-2001 (first entry)

DE Human low density lipoprotein binding protein 2 (LBP-2) cDNA.

KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;

KM atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..654

FT /tag= a

FT /partial

PN WO200164874-A2.

PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US006356.

PR 02-MAR-2000; 2000US-00517849.

PR 14-JUL-2000; 2000US-00616289.

XX (BOST-) BOSTON HEART FOUND INC.

PI Lees AM, Lees RS, Law SM, Arizona AA;

XX WPI; 2001-565505/63.

DR P-PSDB; AAB82803.

XX New isolated low density lipoprotein binding polypeptide for treating,

PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX Example 4; Fig 16; 143pp; English.

XX The present sequence is that of a partial cDNA encoding novel human low

CC density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were

CC isolated from human foetal brain, liver and aorta cDNA libraries using

CC rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in

CC AAH26494, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic

CC acids are among claimed polynucleotides of the invention that encode

CC novel polypeptides capable of binding to native and methylated LDL. Also

CC claimed are isolated LBP polypeptides, and biologically active fragments

CC of producing the LBP. Methods of determining if an animal is at risk for

CC atherosclerosis, methods for evaluating an agent for use in treating

CC atherosclerosis, and methods for treating a cell having an abnormality in

CC structure or metabolism of LBP are claimed. Pharmaceutical compositions

CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions,

CC are also claimed

XX Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;

XX Alignment Scores:

Pred. No.: 0.463 Length: 1208  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-09-976-740-21 (1-11) x AAH26494 (1-1208)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11

Db 67 GTGTCAAGAGGCTCTGTAAGTGCCTCGAGAGTGAC 99

RESULT 7

AAH21860

ID AAH21860 standard; DNA; 1336 BP.

AC AAH21860;

DT 27-MAR-2001 (first entry)

DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.

KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;

KM noctropic; neuroprotective; antiviral; antiarteriosclerotic; hepatotropic;

KW antidiabetic; antiinflammatory; antiviral; vulnery; anticonvulsant;

KM antibacterial; antiparasitic; cardiant; immune disorder;

KW Addison's disease; allergy; autoimmune haemolytic anaemia;

KM autoimmune thyroiditis; diabetes mellitus; Crohn's disease;

KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;

KM cardiovascular disorder; wound healing; neurological disease; ds.

OS Homo sapiens.

PN WO200055173-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US005881.

PR 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

DR P-PSDB; AAB58957.

XX New human breast and ovarian cancer associated gene sequences and the

PT polypeptides encoded by these genes, useful in the prevention, treatment

XX and diagnosis of cancer, immune disorders, cardiovascular disorders and

XX neurological diseases.

XX Claim 1; Page 670-671; 1299pp; English.

XX Sequences AAH21814 - AAH22031 represent DNA sequences encoding human

CC proteins AAB58711 - AAB59128. The DNA and protein sequences are

CC associated with breast and ovarian cancer. Included in the invention are

CC sequences AAH22032 - AAH22040 and AAB59129 which are used in the

CC isolation and characterisation of the DNA and protein sequences of the

CC invention. The breast and ovarian cancer associated DNA, protein, agonist

CC or antagonist sequences exhibit cytostatic; immunosuppressive; noctropic;

CC neuroprotective; antiviral; antiarteriosclerotic; hepatotropic; antidiabetic;

CC antiinflammatory; antiviral; vulnery; anticonvulsant; antidiabetic;

CC antifungal; antiparasitic and cardiant activity. The polynucleotide and

CC protein sequences are used in the diagnosis of cancer, particularly

CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists

CC and agonists may also be used in the diagnosis, prevention and treatment

CC of immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;

CC cardiovascular disorders such as myocardial ischaemia; wound healing;

CC neurological diseases such as cerebral anoxia and epilepsy; and  
 CC infectious diseases  
 XX  
 SQ Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;  
 Alignment Scores:  
 Pred. No.: 0.519 Length: 1336  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-976-740-21 (1-11) x AAF21860 (1-1336)  
 QY 1 ValsergluGlySerGluValProGluSerAsp 11  
 Db 139 GTGTCAGAGGGCTCTGAAGTGTCCCGAGAGTAC 171  
 RESULT 8  
 AAH26489 ID AAH26489 standard; cDNA; 1362 BP.  
 XX AC AAH26489;  
 XX DT 12-NOV-2001 (first entry)  
 XX DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
 XX KM Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;  
 KM atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
 KM ss.  
 XX OS Oryctolagus cuniculus.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..955  
 FT FT /\*tag= a  
 FT FT /partial  
 XX PN MO200164874-A2.  
 XX PD 07-SEP-2001.  
 XX PF 28-FEB-2001; 2001WO-US006356.  
 XX PR 02-MAR-2000; 2000US-00517849.  
 XX PR 14-JUL-2000; 2000US-00616289.  
 XX PA (BOST-) BOSTON HEART FOUND INC.  
 XX PI Lees AM, Lees RS, Law SW, Arizona AA;  
 XX PI WPI; 2001-565505/63.  
 XX DR P-PSDB; AAB82799.  
 XX PT New isolated low density lipoprotein binding polypeptide for treating,  
 PT diagnosing and/or identifying therapeutic agents for atherosclerosis.  
 XX Example 2; Fig 12; 143bp; English.  
 XX  
 CC The present sequence is that of cDNA encoding a portion (see AAB82799) of  
 CC novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA  
 CC was isolated following screening of a rabbit cDNA library for clones  
 CC encoding LBPs that bound to both native low density lipoprotein (LDL) and  
 CC methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The  
 CC invention provides claimed polynucleotides encoding novel polypeptides  
 CC which are capable of binding to native and methylated LDL, the isolated  
 CC polypeptides, termed LBPs, and biologically active fragments and  
 CC analogues of them, as well as expression vectors, cells and methods of  
 CC producing the LBPs. Also claimed are methods of determining if an animal  
 CC is at risk for atherosclerosis, methods for evaluating an agent for use  
 CC in treating atherosclerosis, and methods for treating a cell having an

CC abnormality in structure or metabolism of LBP. Pharmaceutical  
 CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine  
 CC compositions, are also claimed  
 XX  
 SQ Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 0.531 Length: 1362  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0  
 US-09-976-740-21 (1-11) x AAH26489 (1-1362)  
 QY 1 ValsergluGlySerGluValProGluSerAsp 11  
 Db 109 GTGTCGAGGGCTCTCGAGGTGCGAGAGCGAT 141  
 RESULT 9  
 AAH26490 ID AAH26490 standard; cDNA; 1422 BP.  
 XX AC AAH26490;  
 XX DT 12-NOV-2001 (first entry)  
 XX DE Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.  
 XX KM Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit;  
 KM atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
 KM ss.  
 XX OS Oryctolagus cuniculus.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..955  
 FT FT /\*tag= a  
 FT FT /partial  
 XX PN MO200164874-A2.  
 XX PD 07-SEP-2001.  
 XX PF 28-FEB-2001; 2001WO-US006356.  
 XX PR 02-MAR-2000; 2000US-00517849.  
 XX PR 14-JUL-2000; 2000US-00616289.  
 XX PA (BOST-) BOSTON HEART FOUND INC.  
 XX PI Lees AM, Lees RS, Law SW, Arizona AA;  
 XX PI WPI; 2001-565505/63.  
 XX DR P-PSDB; AAB82800.  
 XX PT New isolated low density lipoprotein binding polypeptide for treating,  
 PT diagnosing and/or identifying therapeutic agents for atherosclerosis.  
 XX Example 2; Fig 13; 143bp; English.  
 XX  
 CC The present sequence is that of cDNA encoding a portion (see AAB82800) of  
 CC novel rabbit low density lipoprotein binding protein 3 (LBP-3). The cDNA  
 CC was isolated following screening of a rabbit cDNA library for clones  
 CC encoding LBPs that bound to both native low density lipoprotein (LDL) and  
 CC methyl LDL. A full-length sequence for rabbit LBP-3 cDNA is given in  
 CC AAH26491. The invention provides claimed polynucleotides encoding novel  
 CC polypeptides which are capable of binding to native and methylated LDL,  
 CC the isolated polypeptides, termed LBPs, and biologically active fragments  
 CC and analogues of them, as well as expression vectors, cells and methods  
 CC of producing the LBPs. Also claimed are methods of determining if an  
 CC animal is at risk for atherosclerosis, methods for evaluating an agent





PA (BOST-) BOSTON HEART FOUND INC.  
 XX  
 XX Lees AM, Lees RS, Law SW, Arizona AA;  
 PI  
 XX WPI; 2001-565505/63.  
 DR P-PSDB; AAB82807.  
 XX  
 XX New isolated low density lipoprotein binding polypeptide for treating,  
 PT diagnosing and/or identifying therapeutic agents for atherosclerosis.  
 XX  
 XX Claim 4; Fig 2A; 143pp; English.  
 PS  
 XX  
 CC The present sequence is that of cDNA encoding novel rabbit low density  
 CC lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was  
 CC isolated following screening of a rabbit cDNA library for clones encoding  
 CC LBPs that bound to both native low density lipoprotein (LDL) and methyl  
 CC LDL. The invention provides claimed polynucleotides encoding novel  
 CC polypeptides which are capable of binding to native and methylated LDL,  
 CC the isolated polypeptides, termed LBPs, and biologically active fragments  
 CC and analogues of them, as well as expression vectors, cells and methods  
 CC of producing the LBPs. Also claimed are methods for evaluating an agent  
 CC animal is at risk for atherosclerosis, methods for creating a cell  
 CC for use in treating atherosclerosis, and methods for creating a cell  
 CC having an abnormality in structure or metabolism of LBP. Pharmaceutical  
 CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine  
 CC compositions, are also claimed.  
 XX  
 XX  
 SQ Sequence 2561 BP; 372 A; 937 C; 879 G; 373 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.09 Length: 2561  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 5  
 US-09-976-740-21 (1-11) x AAH26500 (1-2561)  
 QY 1 ValSerGluGlySerGluValProGluSerAsp 11  
 Db 1308 GTGTCGAGGGGCTCGAGGTCGCCGAGAGCGAT 1240  
 RESULT 14  
 AAH26495  
 ID AAH26495 standard; DNA; 12425 BP.  
 XX  
 AC AAH26495;  
 XX  
 DT 12-NOV-2001 (first entry)  
 XX  
 DE Human low density lipoprotein binding protein 2 (LBP-2) gene.  
 XX  
 XX Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
 KM atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
 KM ds.  
 XX  
 XX OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 2832..5153  
 FT /\*tag= a  
 FT /note= "includes introns"  
 FT 2832..3785  
 FT /\*\*tag= b  
 FT 3786..4207  
 FT /\*\*tag= c  
 FT 4208..4502  
 FT /\*\*tag= d  
 FT 4503..4593  
 FT /\*\*tag= e  
 FT 4594..4694  
 FT /\*\*tag= f  
 FT exon

FT intron 4695..4787  
 FT /\*\*tag= g  
 FT 4788..4899  
 FT /\*\*tag= h  
 FT intron 4900..4994  
 FT /\*\*tag= i  
 FT exon 4995..5153  
 FT /\*\*tag= j  
 FN W0200164874-A2.  
 XX  
 XX 07-SEP-2001.  
 XX  
 XX 28-FEB-2001; 2001MO-US006356.  
 XX  
 XX 02-MAR-2000; 2000US-00517849.  
 PR 14-JUL-2000; 2000US-00616289.  
 XX  
 XX (BOST-) BOSTON HEART FOUND INC.  
 PA  
 XX Lees AM, Lees RS, Law SW, Arizona AA;  
 XX  
 XX WPI; 2001-565505/63.  
 DR P-PSDB; AAB82806.  
 XX  
 XX New isolated low density lipoprotein binding polypeptide for treating,  
 PT diagnosing and/or identifying therapeutic agents for atherosclerosis.  
 XX  
 XX  
 ES Example 4; Fig 23; 143pp; English.  
 XX  
 XX The present sequence is that of genomic DNA encoding novel human low  
 CC density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was  
 CC isolated from a human genomic library by screening with LBP-2 cDNA (see  
 CC AAB26494). The open reading frame spans 5 exons. Human LBP-2 nucleic  
 CC acids are among claimed polynucleotides of the invention that encode  
 CC novel polypeptides, termed LBPs, capable of binding to native and  
 CC methylated LDL. Also claimed are isolated LBP polypeptides and  
 CC biologically active fragments and analogues of them, as well as  
 CC expression vectors, cells and methods of producing the LBPs. Methods of  
 CC determining if an animal is at risk for atherosclerosis, and methods for  
 CC evaluating an agent for use in treating atherosclerosis, and methods for  
 CC treating a cell having an abnormality in structure or metabolism of LBP  
 CC are claimed. Pharmaceutical compositions comprising an LBP polypeptide or  
 CC nucleic acid, and vaccine compositions, are also claimed.  
 XX  
 XX  
 SQ Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 6.58 Length: 12425  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 5  
 US-09-976-740-21 (1-11) x AAH26495 (1-12425)  
 QY 1 ValSerGluGlySerGluValProGluSerAsp 11  
 Db 4283 GTGTCGAGGGGCTCGAAGTCCCGAGAGTGATC 4315  
 RESULT 15  
 AAF64847/C  
 ID AAF64847 standard; cDNA; 378 BP.  
 XX  
 AC AAF64847;  
 XX  
 DT 09-APR-2001 (first entry)  
 XX  
 XX Novel human polynucleotide, SEQ ID NO: 603.  
 DE Human; cytosolic; gene therapy; colon cancer; prostate cancer;  
 XX breast cancer; lung cancer; cancer detection; ss.  
 KM



```

XX      Homo sapiens.
OS
XX      WO200102568-A2.
FN
XX      11-JAN-2001.
PD
XX      30-JUN-2000; 2000WO-US018374.
PF
XX      02-JUL-1999; 99US-0142310P.
PR      02-JUL-1999; 99US-0142311P.
XX      (CHIR ) CHIRON CORP.
PA      (HYSE-) HYSEQ INC.
XX
PI      Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J;
PI      Kasam A, Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G;
PI      Drmanac R, Cikenjakov R, Drmanac S, Dickson M, Labat I;
PI      Leshkowitz D, Kita D, Garcia V, Jones LW, Strache-Crain B;
XX
DR      WPI, 2001-091805/10.
XX
PT      Library of polynucleotides for diagnosing a cancerous state of a
PT      mammalian cell and detecting cancer, particularly of the colon or
PT      prostate, comprises 3351 human polynucleotide sequences.
XX
PS      Claim 9; Page 631; 1046pp; English.
XX
CC      The present sequence is one of 3351 sequences in a library of human
CC      polynucleotides. The library is used to detect differentially expressed
CC      genes correlated with a cancerous state of a mammalian cell and can
CC      detect colon, prostate, breast and lung cancer. The library can be used
CC      to produce probes for detection of mRNA and to produce additional copies
CC      of the polynucleotides. The probes can be used for chromosome mapping of
CC      the polynucleotide and for detection of transcription levels. Ribozymes
CC      or antisense oligonucleotides can be generated. The polynucleotides and
CC      their gene products are used as genetic or biochemical markers (e.g. in
CC      blood or tissues) that will detect the earliest changes along the
CC      carcinogenesis pathway and/or monitor the efficacy of therapies and
CC      preventive interventions. The polynucleotides, polypeptides and
CC      antibodies against them can be used in pharmaceutical compositions to
CC      treat the cancers and proliferative disorders such as neoplasia,
CC      dysplasia and hyperplasia
XX
SQ      Sequence 378 BP; 95 A; 95 C; 83 G; 105 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.:      47.3      Length:      378
Score:          41.00     Matches:      8
Percent Similarity: 90.81% Conservative: 2
Best Local Similarity: 72.73% Mismatches: 1
Query Match:     75.93%   Indels:      0
DB:             5        Gaps:       0
US-09-976-740-21 (1-11) x AAF64847 (1-378)
QY      1 ValSerGluGlySerGluValProGluSerasp 11
Db      55 GTCACGAGGAAATTCAGAGGTGTCAGAGCCGAG 23

```

Search completed: March 12, 2004, 21:08:41  
 Job time : 23.4357 secs



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OW protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 20:05:17 ; Search time 3.7295 Seconds  
(without alignments)  
1636.805 Million cell updates/sec

Title: US-09-976-740-21  
Perfect score: 54  
Sequence: 1 VSEGSSEVPESD 11

Scoring table:  
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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 segs, 277475446 residues  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n.model -DEV=x1p  
-Q=/cgn2\_1/USPTO.spool/P/US09976740/runat.10032004.094549.19564/app.query.fasta\_1.1898  
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-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	33	4	US-08-979-608A-32
2	54	100.0	33	4	US-09-517-849-32
3	54	100.0	33	4	US-09-616-289-32
4	54	100.0	36	4	US-08-979-608A-38
5	54	100.0	36	4	US-08-979-608A-38
6	54	100.0	36	4	US-08-979-608A-38
7	54	100.0	36	4	US-08-979-608A-38
8	54	100.0	78	4	US-09-517-849-31
9	54	100.0	78	4	US-09-517-849-31
10	54	100.0	78	4	US-09-616-289-31
11	54	100.0	84	4	US-08-979-608A-37
12	54	100.0	84	4	US-09-517-849-37

13	54	100.0	1208	4	US-08-979-608A-16	Sequence 16, Appl
14	54	100.0	1208	4	US-09-517-849-16	Sequence 16, Appl
15	54	100.0	1208	4	US-09-616-289-16	Sequence 16, Appl
16	54	100.0	1362	4	US-08-979-608A-12	Sequence 12, Appl
17	54	100.0	1362	4	US-09-517-849-12	Sequence 12, Appl
18	54	100.0	1362	4	US-09-616-289-12	Sequence 12, Appl
19	54	100.0	1422	4	US-08-979-608A-13	Sequence 13, Appl
20	54	100.0	1422	4	US-09-517-849-13	Sequence 13, Appl
21	54	100.0	1422	4	US-09-616-289-13	Sequence 13, Appl
22	54	100.0	1617	4	US-08-979-608A-11	Sequence 11, Appl
23	54	100.0	1617	4	US-09-517-849-11	Sequence 11, Appl
24	54	100.0	1617	4	US-09-616-289-11	Sequence 11, Appl
25	54	100.0	1617	4	US-09-616-289-11	Sequence 11, Appl
26	54	100.0	2561	4	US-09-616-289-48	Sequence 48, Appl
27	54	100.0	12425	4	US-09-616-289-50	Sequence 50, Appl
28	39	72.2	6728	4	US-09-674-459B-1	Sequence 1, Appl
29	39	72.2	14759	4	US-09-661-887-1	Sequence 1, Appl
30	38	70.4	411	4	US-09-404-879A-21	Sequence 21, Appl
31	38	70.4	411	4	US-09-338-933-21	Sequence 21, Appl
32	38	70.4	411	4	US-09-338-933-21	Sequence 21, Appl
33	38	70.4	411	4	US-09-215-681-21	Sequence 21, Appl
34	38	70.4	411	4	US-09-215-681-21	Sequence 21, Appl
35	38	70.4	414	4	US-09-404-879A-73	Sequence 73, Appl
36	38	70.4	414	4	US-09-338-933-73	Sequence 73, Appl
37	38	70.4	414	4	US-09-215-681-73	Sequence 73, Appl
38	38	70.4	3090	5	PCT-US93-06251-7	Sequence 7, Appl
39	36	66.7	276	4	US-09-107-532A-65	Sequence 65, Appl
40	36	66.7	1092	4	US-09-107-532A-1437	Sequence 1437, Ap
41	36	66.7	2577	4	US-09-266-464-1	Sequence 1, Appl
42	36	66.7	2577	4	US-09-016-434-1095	Sequence 1095, Ap
43	36	66.7	3267	3	US-08-633-768A-3	Sequence 3, Appl
44	36	66.7	3267	3	US-09-280-197-3	Sequence 3, Appl
45	35.5	65.7	2268	4	US-09-134-000C-3286	Sequence 3286, Ap

ALIGNMENTS

RESULT 1  
US-08-979-608A-32  
Sequence 32, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,330  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...33  
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US-08-979-608A-32

Alignment Scores:  
Pred. No.: 0.0013 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) x US-08-979-608A-32 (1-33)  
Cy 1 ValsergluGlySerGluValProGluSerAsp 11  
Db 1 GTGTCAGAGGGCCTGTGAAGTGCCTGAGAGTGAC 33

RESULT 2  
US-09-517-849-32  
Sequence 32, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-Nov-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...33  
SEQUENCE DESCRIPTION: SEQ ID NO: 32:  
US-09-517-849-32

Alignment Scores:  
Pred. No.: 0.0013 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) x US-09-517-849-32 (1-33)  
Cy 1 ValsergluGlySerGluValProGluSerAsp 11  
Db 1 GTGTCAGAGGGCCTGTGAAGTGCCTGAGAGTGAC 33

RESULT 3  
US-09-616-289-32  
Sequence 32, Application US/09616289  
Patent No. 6632823  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-32

Alignment Scores:  
Pred. No.: 0.0013 Length: 33  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) x US-09-616-289-32 (1-33)  
Cy 1 ValsergluGlySerGluValProGluSerAsp 11  
Db 1 GTGTCAGAGGGCCTGTGAAGTGCCTGAGAGTGAC 33

RESULT 4  
US-08-979-608A-38  
Sequence 38, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/08/979,608  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-979-608A-38

Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59618)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...36  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-08-979-608A-38  
Alignment Scores:  
Pred. No.: 0.00144 Length: 36  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-21 (1-11) x US-08-979-608A-38 (1-36)  
QY 1 Valsergluylsergluvalprogluserasp 11  
Db 4 GTGTCCGAGGCTCGAGGTGCCCCGAGAGCGCAT 36  
RESULT 5  
US-09-517-849-38  
Sequence 38, Application US/09517849  
Patent No. 6603588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...36  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-517-849-38  
Alignment Scores:  
Pred. No.: 0.00144 Length: 36  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-21 (1-11) x US-09-517-849-38 (1-36)  
QY 1 Valsergluylsergluvalprogluserasp 11  
Db 4 GTGTCCGAGGCTCGAGGTGCCCCGAGAGCGCAT 36  
RESULT 6  
US-09-616-289-38  
Sequence 38, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 38  
LENGTH: 36  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-38

## Alignment Scores:

Pred. No.:	0.00144	Length:	36
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-976-740-21 (1-11) x US-09-616-289-38 (1-36)

Cy 1 ValSerGIuGIySerGIuValProGIuSerAsp 11  
DB 4 GTGTCCAGAGGCTCGAGGTGCCGAGACGAT 36

## RESULT 7

US-08-979-608A-31  
Sequence 31, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.

Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-08-979-608A-31

## Alignment Scores:

Pred. No.:	0.00346	Length:	78
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-09-976-740-21 (1-11) x US-08-979-608A-31 (1-78)

Cy 1 ValSerGIuGIySerGIuValProGIuSerAsp 11  
DB 46 GTGTCCAGAGGCTCTCGAAGTCCGAGAGTGAC 78

## RESULT 8

US-09-517-849-31  
Sequence 31, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.

Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-MAR-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-8906  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-517-849-31

Alignment Scores:  
Pred. No.: 0.00346  
Score: 54.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Length: 78  
Matches: 11  
Conservative: 0  
Mismatches: 0  
Indels: 0  
Gaps: 0

US-09-976-740-21 (1-11) X US-09-517-849-31 (1-78)

QY 1 Valsergluylsergluvalprogluserasp 11  
DB 46 GTGTCAAGAGGGCTCTGAAGTGCCTCCGAGAGTGAC 78

RESULT 9  
US-09-616-289-31  
Sequence 31, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14/517,849  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 78  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-31

Alignment Scores:  
Pred. No.: 0.00346 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) X US-09-616-289-31 (1-78)

QY 1 Valsergluylsergluvalprogluserasp 11  
DB 46 GTGTCAAGAGGGCTCTGAAGTGCCTCCGAGAGTGAC 78

RESULT 10  
US-08-979-608A-37  
Sequence 37, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.  
APPLICANT: Lees, Robert S.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
TITLE OF INVENTION: BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..84  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-08-979-608A-37

Alignment Scores:  
Pred. No.: 0.00377 Length: 84  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) X US-08-979-608A-37 (1-84)

QY 1 Valsergluylsergluvalprogluserasp 11  
DB 52 GTGTCAAGAGGGCTCTGAAGTGCCTCCGAGAGTGAC 84

RESULT 11  
US-09-517-849-37  
Sequence 37, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.  
APPLICANT: Lees, Robert S.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
TITLE OF INVENTION: BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-MAR-2000  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..84  
SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-517-849-37

Alignment Scores:  
Pred. No.: 0.00377 Length: 84  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) x US-09-517-849-37 (1-84)  
Qy 1 ValserGluglysergluValProgluSerasp 11  
Db 52 GTGTCCGAGGGCTCGAGAGTGTCCCGAGAGCGAT 84

RESULT 12  
US-09-616-289-37  
Sequence 37, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 37  
LENGTH: 84  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-37

Alignment Scores:  
Pred. No.: 0.00377 Length: 84  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) x US-09-616-289-37 (1-84)  
Qy 1 ValserGluglysergluValProgluSerasp 11  
Db 52 GTGTCCGAGGGCTCGAGAGTGTCCCGAGAGCGAT 84

RESULT 13  
US-08-979-608A-16  
Sequence 16, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-8906  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-08-979-608A-16

Alignment Scores:  
Pred. No.: 0.0775 Length: 1208  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-21 (1-11) x US-08-979-608A-16 (1-1208)  
Qy 1 ValserGluglysergluValProgluSerasp 11  
Db 67 GTGTCCGAGGGCTCGAGAGTGTCCCGAGAGCGAT 99



RESULT 14  
US-09-517-849-16  
Sequence 16, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon M.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-517-849-16  
Alignment Scores:  
Pred. No.: 0.0775 Length: 1208  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-09-976-740-21 (1-11) x US-09-517-849-16 (1-1208)  
QY 1 ValSerGluGlySerGluValProGluSerAsp 11  
DB 67 GTGTCAAGAGGCTCTGAAGTGCCTCCGAGAGTGAC 99  
RESULT 15  
US-09-616-289-16  
Sequence 16, Application US/09616289  
Patent No. 6632323  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-09-616-289-16  
Alignment Scores:  
Pred. No.: 0.0775 Length: 1208  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-09-976-740-21 (1-11) x US-09-616-289-16 (1-1208)  
QY 1 ValSerGluGlySerGluValProGluSerAsp 11  
DB 67 GTGTCAAGAGGCTCTGAAGTGCCTCCGAGAGTGAC 99  
Search completed: March 13, 2004, 04:06:26  
Job time : 5.7295 secs





SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/962,055

FILING DATE: 24-Sep-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,608

FILING DATE: 26-NOV-1997

APPLICATION NUMBER: US 60/031,930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...33

SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-962-055-32

Alignment Scores:

Pred. No.:	0.00499	Length:	33
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-21 (1-11) x US-09-962-055-32 (1-33)

Qy 1 Valsergluylsergluvalprogluserasp 11

Db 1 GTGTCAAGGGGCTCTGAAGTGCCTGAGAGTGCAC 33

RESULT 2

US-09-976-740-32

Sequence 32, Application US/09976740

Publication No. US20020194633A1

GENERAL INFORMATION:

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Atjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 32

LENGTH: 33

TYPE: DNA

ORGANISM: Homo sapiens

US-09-976-740-32

Alignment Scores:

Pred. No.:	0.00499	Length:	33
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-21 (1-11) x US-09-976-740-32 (1-33)

Qy 1 Valsergluylsergluvalprogluserasp 11

Db 1 GTGTCAAGGGGCTCTGAAGTGCCTGAGAGTGCAC 33

RESULT 3

US-10-671-242-32

Sequence 32, Application US/10671242

Publication No. US20040040049A1

GENERAL INFORMATION:

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Atjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/10/671,242

CURRENT FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: US/09/616,289

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608

PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547

PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 32

LENGTH: 33

TYPE: DNA

ORGANISM: Homo sapiens

US-10-671-242-32

Alignment Scores:

Pred. No.:	0.00499	Length:	33
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-10-023-529-32

Sequence 32, Application US/10023529

Publication No. US20020129388A1

GENERAL INFORMATION:

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Atjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-529-32

## Alignment Scores:

Pred. No.:	0.00499	Length:	33
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0

US-09-976-740-21 (1-11) x US-10-023-529-32 (1-33)

Qy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 1 GTGTCAAGAGGGCTCTGAAGTCCCGAGAGTGAC 33

## RESULT 5

US-10-023-523-32  
Sequence 32, Application US/10023523  
Publication No. US20020152485A1  
GENERAL INFORMATION:

APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
AND TREATING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,523  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-523-32

## Alignment Scores:

Pred. No.:	0.00499	Length:	33
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0

Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-976-740-21 (1-11) x US-10-023-523-32 (1-33)

Qy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 1 GTGTCAAGAGGGCTCTGAAGTCCCGAGAGTGAC 33

## RESULT 6

US-10-616-187-32  
Sequence 32, Application US/10616187  
Publication No. US20040013668A1  
GENERAL INFORMATION:

APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
AND TREATING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/616,187  
CURRENT FILING DATE: 2003-07-09  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 32  
LENGTH: 33  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-616-187-32

## Alignment Scores:

Pred. No.:	0.00499	Length:	33
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	15	Gaps:	0

US-09-976-740-21 (1-11) x US-10-616-187-32 (1-33)

Qy 1 ValsergluGlySerGluValProgluSerasp 11  
Db 1 GTGTCAAGAGGGCTCTGAAGTCCCGAGAGTGAC 33

## RESULT 7

US-09-962-055-38  
Sequence 38, Application US/09962055  
Patent No. US20020052033A1  
GENERAL INFORMATION:

APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street

```

; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,055
; FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..36
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-962-055-38

Alignment Scores:
Pred. No.: 0.00543 Length: 36
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-976-740-21 (1-11) x US-09-962-055-38 (1-36)
QY 1 ValsergluGlySerGluValProGluSerAsp 11
Db 4 GTGTCCGAGGGCTCGAGGTGCCCCGAGAGCGCAT 36

RESULT 8
US-09-976-740-38
; Sequence 38, Application US/09/976740
; Publication No. US20020194633A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Amibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976,740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-976-740-38

Alignment Scores:
Pred. No.: 0.00543 Length: 36
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 9

US-09-976-740-21 (1-11) x US-09-976-740-38 (1-36)
QY 1 ValsergluGlySerGluValProGluSerAsp 11
Db 4 GTGTCCGAGGGCTCGAGGTGCCCCGAGAGCGCAT 36

RESULT 9
US-10-671-242-38
; Sequence 38, Application US/10671242
; Publication No. US20040040049A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Amibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671,242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-671-242-38

Alignment Scores:
Pred. No.: 0.00543 Length: 36
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 12

US-09-976-740-21 (1-11) x US-10-671-242-38 (1-36)
QY 1 ValsergluGlySerGluValProGluSerAsp 11
Db 4 GTGTCCGAGGGCTCGAGGTGCCCCGAGAGCGCAT 36

RESULT 10
US-10-023-529-38
; Sequence 38, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/10/023,529
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-023-529-38

Alignment Scores:
Pred. No.: 0.00543 Length: 36
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-976-740-21 (1-11) x US-10-023-529-38 (1-36)
; Sequence 38, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/10/023,523
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-023-523-38

RESULT 11
QY 1 ValSerGluGlySerGluValProGluSerAsp 11
Db 4 GTGTCCGAGGCTCGAGGTGCCCCGAGAGCGCAT 36
```

```

; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/10/023,529
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-023-523-38

Alignment Scores:
Pred. No.: 0.00543 Length: 36
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-976-740-21 (1-11) x US-10-023-523-38 (1-36)
; Sequence 38, Application US/09962055
; Patent No. US20020052033A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; FILE REFERENCE: 10797-004001
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/10/616,187
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-023-523-38

RESULT 12
QY 1 ValSerGluGlySerGluValProGluSerAsp 11
Db 4 GTGTCCGAGGCTCGAGGTGCCCCGAGAGCGCAT 36
```

# BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-962-055-31  
Alignment Scores:  
Pred. No.: 0.0116 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 9  
US-09-976-740-21 (1-11) x US-09-962-055-31 (1-78)  
QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
Db 46 GTGTCAAGAGGGCTCTGTGAAGTCCGAGAGTGAC 78  
RESULT 14  
US-09-976-740-31  
Sequence 31, Application US/09976740  
Publication No. US20020194633A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.  
APPLICANT: Arijona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/976,740  
FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 78  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-976-740-31  
Alignment Scores:  
Pred. No.: 0.0116 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 9  
US-09-976-740-21 (1-11) x US-09-976-740-31 (1-78)  
QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
Db 46 GTGTCAAGAGGGCTCTGTGAAGTCCGAGAGTGAC 78  
RESULT 15  
US-10-671-242-31  
Sequence 31, Application US/10671242  
Publication No. US20040040049A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.  
APPLICANT: Arijona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/671,242  
FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 78  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-671-242-31  
Alignment Scores:  
Pred. No.: 0.0116 Length: 78  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 12  
US-09-976-740-21 (1-11) x US-10-671-242-31 (1-78)  
QY 1 ValSerGIuGIySerGIuValProGIuSerASP 11  
Db 46 GTGTCAAGAGGGCTCTGTGAAGTCCGAGAGTGAC 78



Mon Mar 15 09:28:14 2004

us-09-976-740-21.rnpb

Page 7

Db 46 GTGTCAGAGGGGCTCTGTGAAGTGGCCCGAGAGTGC 78

Search completed: March 13, 2004, 04:26:14  
Job time : 15.9143 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:55:37 ; Search time 166.319 Seconds

(without alignments)  
1975.018 Million cell updates/sec

Title: US-09-976-740-21  
Perfect score: 54  
Sequence: 1 VSBSSEVPESD 11

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1p  
-Q/cgm2\_1/USBP2.spool p/US09976740/runat\_10032004\_094548\_19551/app.query.fasta\_1.1898  
-DB=EST -QMT=fastcap -SUFFIX=rev -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09976740 @CGN 1.1 10232 @runat\_10032004\_094548\_19551 -NCPV=6 -ICPV=3  
-NO MAP -LARGOITRY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_huv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vit:\*  
28: gb\_gss1:\*

29: gb\_gss2:.\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Match Length	DB	ID	Description
1	54	100.0	222	9	AA807020
2	54	100.0	253	9	AI713567
3	54	100.0	269	9	AA029068
4	54	100.0	271	9	AA765474
5	54	100.0	274	12	BT004562
6	54	100.0	275	9	AA806888
7	54	100.0	278	9	AA810871
8	54	100.0	284	9	AA766034
9	54	100.0	289	9	AA804533
10	54	100.0	302	9	AI137809
11	54	100.0	302	10	BF194967
12	54	100.0	322	9	AI470106
13	54	100.0	324	10	BF806978
14	54	100.0	325	10	BE100055
15	54	100.0	325	10	BE112745
16	54	100.0	328	10	BF561482
17	54	100.0	340	9	AI711065
18	54	100.0	342	9	AI172508
19	54	100.0	345	10	BF944758
20	54	100.0	348	9	AI548990
21	54	100.0	349	10	BE114632
22	54	100.0	367	9	AA769505
23	54	100.0	375	9	AA649303
24	54	100.0	383	10	AA845391
25	54	100.0	384	9	AA836383
26	54	100.0	386	9	AA766164
27	54	100.0	395	10	BE111716
28	54	100.0	407	10	AA594381
29	54	100.0	436	9	AI230441
30	54	100.0	406	9	AI230436
31	54	100.0	412	10	AA134620
32	54	100.0	424	10	AA740100
33	54	100.0	428	9	AA944363
34	54	100.0	429	9	AI097526
35	54	100.0	430	9	AI548989
36	54	100.0	430	10	AA142485
37	54	100.0	436	9	AI556877
38	54	100.0	436	10	AA490346
39	54	100.0	439	9	AI102597
40	54	100.0	446	9	AI179283
41	54	100.0	451	9	AA016794
42	54	100.0	453	10	AA531666
43	54	100.0	453	10	BE199810
44	54	100.0	455	9	AA827627
45	54	100.0	455	9	AI186973

## ALIGNMENTS

RESULT 1  
AA807020  
LOCUS  
DEFINITION  
AA807020 222 bp mRNA linear EST 07-APR-1998  
cc30g04.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:135124 3'  
similar to contig element M81 repetitive element ;, mRNA  
sequence.  
ACCESSION  
AA807020 GI:2876596  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 222)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLN at:  
[www.bio.linn.gov/bdnp/image.html](http://www.bio.linn.gov/bdnp/image.html)  
 Insert Length: 1153 Std Error: 0.00  
 Seq primer: -40m13 fwd. RT from Amersham  
 High quality sequence stop: 211.  
 Location/Qualifiers  
 1..222  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1351254"  
 /tissue\_type="germinal center B cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP GCBI"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
 was prepared from human tonsillar cells enriched for  
 germinal center B cells by flow sorting (CD20+, IgD-),  
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
 primed with a Not I - oligo(dT) primer  
 [5'-TGTTACATCTGAGAGCGGCGCTCATTTTCTTTTCTTTT-3'  
 ]. Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified p773 vector. Library  
 was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.37 Length: 222  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x AA807020 (1-222)

CY 1 ValSerGluGlySerGluValProGluSerAsp 11  
 DB 124 GTGTGAGAGGGCTCTGAGTGCCTCCGAGAGTGAC 156

RESULT 2  
 LOCUS A1713567 253 bp mRNA linear EST\_08-JUN-1999  
 DEFINITION UI-R-AG1-aan-a-08-0-UI.s1 UI-R-AG1 Rattus norvegicus cDNA clone  
 ACCESSION A1713567  
 VERSION A1713567  
 KEYWORDS GI:5017367  
 SOURCE EST.  
 ORGANISM Rattus norvegicus (Norway rat)  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 253)  
 REFERENCE Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 AUTHORS Normalization and subtraction: two approaches to facilitate gene

JOURNAL discovery  
 MEDLINE Genome Res. 6 (9), 791-806 (1996)  
 PUBMED 9704447  
 8889548  
 COMMENT Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
 Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA library Preparation: M.B.  
 Soares Lab Clone distribution: clones will be available through  
 Research Genetics ([www.resgen.com](http://www.resgen.com)) The following repetitive  
 elements were found in this cDNA sequence: 93-134,  
 >GC richflow complexity 135-216, >(GGA)n#simple\_repeat  
 Seq primer: M13 Forward  
 POLY(A)-NO.

FEATURES  
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 1..253  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-AG1-aan-a-08-0-UI"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="UI-R-AG1"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-AG1  
 library is a normalized library constructed from 13 dpc  
 rat ventricle. The tag is a string of 6 nucleotides  
 present between the Not I site and the oligo-dT track.  
 The library was constructed as described by Bonaldo,  
 Lennon and Soares, Genome Research 6: 791-806, 1996.  
 Tissue provided by Jim Lin, Department of Biology,  
 University of Iowa.  
 TAG\_TISSUE=atrium at 16.5 dpc  
 TAG\_LIB=UI-R-AG1  
 TAG\_SEQ=GATTC"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.98 Length: 253  
 Score: 54.00 Matches: 11  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x A1713567 (1-253)

CY 1 ValSerGluGlySerGluValProGluSerAsp 11  
 DB 221 GTATCTGAGGGCTCTGAGAGTGCCTCCGAGAGTGAC 253

RESULT 3  
 LOCUS AA029068 269 bp mRNA linear EST\_09-MAY-1997  
 DEFINITION ZK09807.s1 Soares.Pregnant.uterus.NbH9U Homo sapiens cDNA clone  
 ACCESSION AA029068  
 VERSION AA029068  
 KEYWORDS GI:1496470  
 SOURCE EST.  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 269)  
 REFERENCE Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
 Chissee,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,  
 Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

**TITLE**  
JOURNAL MEDLINE  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
8889549  
PUBMED

**COMMENT**  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: polyT not found  
Insert length: 1135 Std Error: 0.00  
Seq primer: -40m13 fwd from Amersham  
High quality sequence stop: 229.  
Location/Qualifiers

# FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3756079"  
/db\_xref="taxon:9606"  
/clone="IMAGE:470077"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Scars pregnant uterus NBHPU"  
/note="Organ: uterus; Vector: pT73-Pac; Site 1: Not I;  
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -  
oligo(dT) primer [5'-  
AAGTGAAGAATTGCGCGCCCTTTTCTTTTCTTTT 3']  
double-stranded cDNA was ligated to Eco RI adaptors  
(pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by M. Fatima Bernaldo."

## ORIGIN

**Alignment Scores:**  
Pred. No.: 4.3 Length: 269  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x AA029068 (1-269)

**QY**  
1 ValSerGluGlySerGluValProGluSerAsp 11  
|||||  
Db 169 GTGTCAAGAGGCTCTGAAGTCCCGAGAGTGAC 201

**RESULT 4**  
AA765474 271 bp mRNA linear EST 08-FEB-1998  
AA765474  
LOCUS  
DEFINITION  
OA03d01.s1 NCI CGAP GCB1 Homo sapiens CDNA clone IMAGE:1303873 3'  
similar to contains\_Alu repetitive element; contains element MER22  
repetitive element; mRNA sequence.  
AA765474.1 GI:2816712  
EST.

**ACCESSION**  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE

AA765474  
AA765474  
AA765474.1 GI:2816712  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bernaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www.bio.llnl.gov/bhrp/image/image.html](http://www.bio.llnl.gov/bhrp/image/image.html)  
Insert length: 1136 Std Error: 0.00  
Seq primer: -40m13 fwd. Et from Amersham  
High quality sequence stop: 269.  
Location/Qualifiers

# FEATURES

## source

1. 271  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1303873"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GCB1"  
/note="Vector: pT73-Pac (pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD+),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCATCTGAAGTGGAGCGCCCTCTTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bernaldo."

## ORIGIN

**Alignment Scores:**  
Pred. No.: 4.34 Length: 271  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x AA765474 (1-271)

**QY**  
1 ValSerGluGlySerGluValProGluSerAsp 11  
|||||  
Db 127 GTGTCAAGAGGCTCTGAAGTCCCGAGAGTGAC 159

**RESULT 5**  
B1004562 274 bp mRNA linear EST 13-JUN-2001  
B1004562  
LOCUS  
DEFINITION  
MR4-HN0054-070301-002-g04 HN0054 Homo sapiens CDNA, mRNA sequence.  
B1004562  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

**REFERENCE**  
AUTHORS  
TITLE

B1004562  
B1004562  
B1004562.1 GI:14408636  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 274)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,  
Nagai, M.A., da Silva, M., Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bais, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Congenel, C.V.,  
O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL:  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&cl2=MR4-IN0054-  
070301-002-904&cl3=2001-03-07&cl4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 39  
High quality sequence stop: 274.  
Location/Qualifiers

## FEATURES

## source

1..274  
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/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="HN0054"  
/note="Organ: head normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI. A mini-library was made by cloning products  
derived from ORSTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.4 Length: 274  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-976-740-21 (1-11) x BI004562 (1-274)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11

Db 206 GTGTCAAGAGGGCTCTGAAGTCCCGAGAGTGAC 174

RESULT 6 AA806888 275 bp mRNA linear EST 07-APR-1998  
LOCUS cc32906.s1 NCI CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1351450 3'

DEFINITION similar to contains element TAR1 repetitive element ;, mRNA  
sequence.

ACCESSION AA806888  
VERSION AA806888.1 GI:2876464

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 275)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

JOURNAL  
AUTHORS  
TITLE  
COMMENT

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
www-bio.linn.gov/bdrip/image/image.html  
Insert Length: 1112 Std Error: 0.00  
Seq primer: -40ml3 fwd. Et from Amersham  
High quality sequence stop: 229.  
Location/Qualifiers

## FEATURES

## source

1..275  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1351450"  
/tissue\_type="germinal center B cell"  
/lab\_host="BDH108"  
/clone\_lib="NCI-CGAP\_GCB1"  
/note="Vector: pRT3D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGGGGCTCATTTTCTTTTCTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pRT3D vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.42 Length: 275  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x AA806888 (1-275)

Qy 1 ValSerGluGlySerGluValProGluSerAsp 11

Db 130 GTGTCAAGAGGGCTCTGAAGTCCCGAGAGTGAC 162

RESULT 7 AA810871 278 bp mRNA linear EST 19-FEB-1998  
LOCUS cb44905.s1 NCI CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1336184 3'

DEFINITION similar to contains element PTR7 repetitive element ;, mRNA  
sequence.

ACCESSION AA810871  
VERSION AA810871.1 GI:2880482

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 278)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnl.gov/bbrrp/image/image.html  
Insert Length: 1143 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 269.  
Location/Qualifiers

FEATURES  
source  
1..278  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1336184"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GCBI"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.48 Length: 278  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x AA810871 (1-278)

QY 1 ValSerGIUGISerGIuValProGIuSerASP 11  
Db 127 GTGTCAAGAGGGCTCTGAAGTGGCGAGAGTGAC 159

RESULT 8 284 bp mRNA linear EST 08-FEB-1998  
AA766034 284 bp mRNA linear EST 08-FEB-1998  
LOCUS 041509.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1305017 3'  
DEFINITION similar to contains element MER22 repetitive element ;, mRNA  
sequence.

ACCESSION AA766034  
VERSION AA766034.1 GI:2817272  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 284)  
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.lnl.gov/bbrrp/image/image.html  
Insert Length: 1100 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 283.  
Location/Qualifiers

FEATURES  
source  
1..284  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1305017"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GCBI"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCCCTCATTTTCTTTTCTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.6 Length: 284  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-21 (1-11) x AA766034 (1-284)

QY 1 ValSerGIUGISerGIuValProGIuSerASP 11  
Db 126 GTGTCAAGAGGGCTCTGAAGTGGCGAGAGTGAC 158

RESULT 9 289 bp mRNA linear EST 18-FEB-1998  
AA804533 289 bp mRNA linear EST 18-FEB-1998  
LOCUS ns28c06.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1184938 3'  
DEFINITION similar to contains element MER22 repetitive element ;, mRNA  
sequence.

ACCESSION AA804533  
VERSION AA804533.1 GI:2873664  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 289)  
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapsb@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.lnl.gov/bbrrp/image/image.html  
Insert Length: 1490 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 271.  
Location/Qualifiers

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1184938"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI_CGAP GCBI"
/notes="vector: p773D-Pac (pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman
(NCI) and Dr. Gerald Mari (CBER). cDNA synthesis was
primed with a Not I - oligo (dT) primer.
5'-TGTTACCACTCGAGAGCGCGCCGCTCATTTTCTTTTCTTTT-3'
1. Double-stranded cDNA was ligated to Eco RI adaptors
(pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

## ORIGIN

## Alignment Scores:

```

Pred. No.: 4.7 Length: 289
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

```

US-09-976-740-21 (1-11) x AA804533 (1-289)

```

QY 1 ValSerGluGlySerGluValProGluSerASP 11
DB 87 GTGTCTGAGAGCGCTCTGAGTGCCTCGAGAGTGAC 119

```

## RESULT 10

```

LOCUS A1137809 302 bp mRNA linear EST 05-JUL-1999
DEFINITION UI-R-CO-hz-h-01-0-UI.s1 UI-R-CO Rattus norvegicus cDNA clone
A1137809
VERSION A1137809.1 GI:3638586
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 302)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery.
Genome Res. 6 (9), 791-806 (1996)
JOURNAL MEDLINE
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
TEL: 319 335 8250
FAX: 319 335 9565
Email: bento-soares@uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LBNL (info@image.lbl.gov). IMAGE
ID=1782042 The following repetitive elements were found in this
cDNA sequence: 93-134, >GC_richFlow_complexity 135-216,
>(GGA)n#Simple_repeat
Seq primer: M13 Forward
POLYA=No.

```

## FEATURES

## source

## Location/Qualifiers

```

1..302
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CO-hz-h-01-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CO"
/notes="vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CO
library is a subtracted library derived from the UI-R-A1
and UI-R-E1 libraries. The UI-R-A1 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle. The UI-R-E1
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified cDNA inserts from a
pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
been derived was used as a driver in a hybridization with
the pooled UI-R-A1 and UI-R-E1 library in the form of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-CO
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
1996)"

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 4.97 Length: 302
Score: 54.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

```

US-09-976-740-21 (1-11) x A1137809 (1-302)

```

QY 1 ValSerGluGlySerGluValProGluSerASP 11
DB 221 GTATCTGAGCGCTCTGAGAGTGCCTCGAGAGTGAC 253

```

## RESULT 11

```

LOCUS BF194967 302 bp mRNA linear EST 03-NOV-2000
DEFINITION 7c91b05.x1 NCI CGAP OV18 Homo sapiens cDNA clone IMAGE:3643712 3'
sequence.
similar to contains element TAR1 TAR1 repetitive element'', mRNA
sequence.
ACCESSION BF194967
VERSION BF194967.1 GI:11081346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 302)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgs@pds-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento

```



Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LML, send email to: info@image.lml.gov.

FEATURES  
 source  
 Location/Qualifiers

1. 302  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3643712"  
 /issue\_type="fibrosarcoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_id="NCI-CGAP\_Ov18"  
 /note="Organ: Ovary; Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'] TGTACCAATCTGAAGTGGAGCGCGCGGACATTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.97	Length:	302
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-976-740-21 (1-11) x BF194967 (1-302)

Oy 1 ValSerGluGlySerGluValProGluSerasp 11  
 |||||  
 Db 213 GTGTCAAGGGCTCTGAGTCCCGAGAGTGAC 245

RESULT 12  
 LOCUS A1470106 322 bp mRNA linear EST 14-APR-1999

DEFINITION U90909.X1 Soares NSF P8 9M OT PA P S1 Homo sapiens cDNA clone IMAGE:2148832.3, similar to contains TRAI.b2 PTR5 repetitive element, mRNA sequence.

ACCESSION A1470106  
 VERSION A1470106.1 GI:4332196  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 322)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov

THIS clone is available royalty-free through LML; contact the IMAGE Consortium ([info@image.lml.gov](mailto:info@image.lml.gov)) for further information.  
 Insert Length: 387 Std Error: 0.00  
 Seq primer: -40UP from Gibco.

FEATURES  
 source

1. 322  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2148832"  
 /lab\_host="DH10B"  
 /clone\_id="Soares NSF P8 9M OT PA P S1"  
 /note="Organ: pooled; Vector: pTV73D-Pac (Pharmacia) with

## ORIGIN

## Alignment Scores:

Pred. No.:	5.39	Length:	322
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-21 (1-11) x A1470106 (1-322)

Oy 1 ValSerGluGlySerGluValProGluSerasp 11  
 |||||  
 Db 197 GTGTCAAGGGCTCTGAGTCCCGAGAGTGAC 229

RESULT 13  
 LOCUS BF806978 324 bp mRNA linear EST 12-JAN-2001

DEFINITION QV4-C10151-091100-522-a05 C10151 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF806978  
 VERSION BF806978.1 GI:12135967  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 324)  
 Dias Neto E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE  
 PubMed 10737800

COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?l=C10151-091100-522-a05&cl=2000-11-09&cl=1>  
 Seq primer: puc 18 forward  
 High quality sequence stop: 324.

## FEATURES

source

1. 324  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"

/dev\_stage="Adult"  
/clone\_lib="C10151"  
/note="Organ: colon\_ins; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTRYS PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Alignment Scores:  
Pred. No.: 5.43 Length: 324  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-976-740-21 (1-11) x BF806978 (1-324)

QY 1 ValserGlucylserGluValProGluSerAsp 11  
DB 92 GTCTCAGAGGCTGTGAAGTCCCGAGAGTGAC 124

RESULT 14  
LOCUS BE100055 325 bp mRNA linear EST 13-JUN-2000  
DEFINITION UI-R-BJ1-atm-b-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone  
ACCESSION BE100055  
VERSION BE100055.1 GI:8491941  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 325)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Oligo-dt track not found. Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library preparation: M.B.  
Soares Lab Clone distribution: clones will be available through  
Research Genetics (www.resgen.com) The following repetitive  
elements were found in this cDNA sequence: 93-134,  
>GC rich flow complexity 135-216, >(GGA)n#simple\_repeat  
Seq primer: M13 Forward  
POLYA=No.

FEATURES  
source

Location/Qualifiers  
1..325  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-BJ1-atm-b-09-0-UI"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-BJ1"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-BJ1  
library is a subtracted library derived from the following  
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV

canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,  
AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.  
For a detailed description of the library from which this  
clone was derived, please visit our web site at  
rategs.eng.uiowa.edu. The subtraction has been previously  
described in (Bonaldo, Lennon and Soares, Genome Research  
6:791-806, 1996)  
TAG\_SEQ=None found"

## ORIGIN

Alignment Scores:  
Pred. No.: 5.45 Length: 325  
Score: 54.00 Matches: 11  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-976-740-21 (1-11) x BE100055 (1-325)

QY 1 ValserGlucylserGluValProGluSerAsp 11  
DB 221 GTATCTAGAGGCTCGAAGTCCCGAGAGTGAC 253

RESULT 15  
LOCUS BE112745 325 bp mRNA linear EST 13-JUN-2000  
DEFINITION UI-R-BJ1-avo-c-12-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone  
ACCESSION BE112745  
VERSION BE112745.1 GI:8504850  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 325)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Oligo-dt track not found. Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA library preparation: M.B.  
Soares Lab Clone distribution: clones will be available through  
Research Genetics (www.resgen.com) The following repetitive  
elements were found in this cDNA sequence: 93-134,  
>GC rich flow complexity 135-216, >(GGA)n#simple\_repeat  
Seq primer: M13 Forward  
POLYA=No.

FEATURES  
source

Location/Qualifiers  
1..325  
/organism="Rattus norvegicus"  
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/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-BJ1-avo-c-12-0-UI"  
/lab\_host="DH10B (Life Technologies)"  
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/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-BJ1  
library is a subtracted library derived from the following  
tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV  
canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,

AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.  
For a detailed description of the library from which this  
clone was derived, please visit our web site at  
rateest.eng.uiowa.edu. The subtraction has been previously  
described in (Bonaldi, Lennon and Soares, Genome Research  
6:791-806, 1996)  
TAG\_SEQ=None found"

# ORIGIN

## Alignment Scores:

Pred. No.:	5.45	Length:	325
Score:	54.00	Matches:	11
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-976-740-21 (1-11) x BB112745 (1-325)

Qy	1	VaISerGIuGIySerGIuValProGIuSerasp	11
Db	221	GTATCTGAGGGCTCGAAGTGTCCCGAAGGTGAC	253

Search completed: March 13, 2004, 04:01:41  
Job time : 171.319 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:49:56 ; Search time 151.885 Seconds  
(Without alignments)  
2853.675 Million cell updates/sec

Title: US-09-976-740-22  
Perfect score: 58  
Sequence: 1 EDDDDPGFLG 10

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6340544

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xip  
-O=/cgm2.1/USFTO.spool.p/US09976740/runat.10032004.094548.19540/app.query.fasta\_1.1898  
-DB=GenEmbl -GPMT=fastap -SUFFIX=xge -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pcc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09976740 @CGN 1.1 9705 @runat.10032004.094548.19540 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGOUTERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl: \*  
1: gb Da: \*  
2: gb Htg: \*  
3: gb In: \*  
4: gb Om: \*  
5: gb Ov: \*  
6: gb Pat: \*  
7: gb Pl: \*  
8: gb Pr: \*  
9: gb Ro: \*  
10: gb Sts: \*  
11: gb Sts: \*  
12: gb Sts: \*  
13: gb Sts: \*  
14: gb Sts: \*  
15: gb Sts: \*  
16: gb Sts: \*  
17: gb Sts: \*  
18: gb Sts: \*  
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20: gb Sts: \*  
21: gb Sts: \*  
22: gb Sts: \*  
23: gb Sts: \*  
24: gb Sts: \*  
25: gb Sts: \*  
26: gb Sts: \*  
27: gb Sts: \*  
28: gb Sts: \*

29: em Vi: \*  
30: em Htg hum: \*  
31: em Htg Inv: \*  
32: em Htg Other: \*  
33: em Htg Mus: \*  
34: em Htg Pln: \*  
35: em Htg Rod: \*  
36: em Htg Mam: \*  
37: em Htg Vrt: \*  
38: em Sy: \*  
39: em Htg hum: \*  
40: em Htg Mus: \*  
41: em Htg Other: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	30	6	AR199541 Sequence
2	58	100.0	30	6	AR374693 Sequence
3	58	100.0	30	6	AR409328 Sequence
4	58	100.0	30	6	AR439590 Sequence
5	58	100.0	30	6	BD056455 Novel Low
6	58	100.0	425	6	AR418294 Sequence
7	58	100.0	982	9	BD113847 EST and e
8	58	100.0	1134	6	BD275342 49 Human
9	58	100.0	1208	6	AR199535 Sequence
10	58	100.0	1208	6	AR374687 Sequence
11	58	100.0	1208	6	AR409322 Sequence
12	58	100.0	1208	6	AX239573 Sequence
13	58	100.0	1208	6	BD056449 Novel Low
14	58	100.0	1208	6	BC030129 Homo sapi
15	58	100.0	1470	9	AR409337 Sequence
16	58	100.0	1614	6	AX239602 Sequence
17	58	100.0	1617	9	AY453840 Homo sapi
18	58	100.0	12425	6	AR409341 Sequence
19	58	100.0	12425	6	AX239607 Sequence
20	58	100.0	215265	2	AC134005 Rattus no
21	58	100.0	237931	9	AC022098 Homo sapi
22	58	100.0	279020	2	AC133803 Rattus no
23	58	100.0	1362	6	AR199531 Sequence
24	58	100.0	1362	6	AR374683 Sequence
25	58	100.0	1362	6	AR409318 Sequence
26	58	100.0	1362	6	AX239569 Sequence
27	58	100.0	1362	6	BD056445 Novel Low
28	58	100.0	1422	6	AR199532 Sequence
29	58	100.0	1422	6	AR374684 Sequence
30	58	100.0	1422	6	AR409319 Sequence
31	58	100.0	1422	6	AX239570 Sequence
32	58	100.0	1422	6	BD056446 Novel Low
33	58	100.0	1617	6	AR199530 Sequence
34	58	100.0	1617	6	AR374682 Sequence
35	58	100.0	1617	6	AR409317 Sequence
36	58	100.0	1617	6	AX239568 Sequence
37	58	100.0	1617	6	BD056444 Novel Low
38	58	100.0	2560	4	AY453841 Oryctolag
39	58	100.0	2561	6	AR409339 Sequence
40	58	100.0	2561	6	AX239605 Sequence
41	58	100.0	140795	2	AC079562 Mus muscu
42	58	100.0	219687	2	AC079501 Mus muscu
43	58	100.0	1376	8	AK063989 Oryza sat
44	58	100.0	2291	8	AK102006 Oryza sat
45	58	100.0	2291	8	AK102006 Oryza sat

#### ALIGNMENTS

RESULT 1

AR199541  
LOCUS AR199541 30 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 33 from patent US 6355451.  
ACCESSION AR199541  
VERSION AR199541.1 GI:20249615  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 33 12-MAR-2002;  
FEATURES  
source location/Qualifiers  
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/mol\_type="unassigned DNA"

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Pred. No.: 0.0138 Length: 30  
Score: 58.00 Matches: 10  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AR199541 (1-30)

QY 1 GluAspAspProAspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTTAGGC 30

RESULT 2  
LOCUS AR374693 30 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 33 from patent US 6605588.  
ACCESSION AR374693  
VERSION AR374693.1 GI:40077508  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 33 12-AUG-2003;  
FEATURES  
source location/Qualifiers  
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Alignment Scores:  
Pred. No.: 0.0138 Length: 30  
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US-09-976-740-22 (1-10) x AR374693 (1-30)

QY 1 GluAspAspProAspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTTAGGC 30

RESULT 3  
LOCUS AR409328 30 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 33 from patent US 6632923.

ACCESSION AR409328  
VERSION AR409328.1 GI:40160116  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 33 14-OCT-2003;  
FEATURES  
source location/Qualifiers  
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ORIGIN  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AR409328 (1-30)

QY 1 GluAspAspProAspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTTAGGC 30

RESULT 4  
LOCUS AX239590 30 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 33 from Patent WO0164874.  
ACCESSION AX239590  
VERSION AX239590.1 GI:15797266  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in diagnosing  
and treating atherosclerosis  
JOURNAL Patent: WO 0164874-A 33 07-SEP-2001;  
FEATURES  
source location/Qualifiers  
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/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.0138 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AX239590 (1-30)

QY 1 GluAspAspProAspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTTAGGC 30

RESULT 5  
LOCUS BD056455 30 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel low density lipoprotein binding proteins and their use in

diagnosing and treating atherosclerosis.  
ACCESSION BD056455  
VERSION BD056455.1 GI:22602061  
KEYWORDS JP 2001506983-A/13.  
SOURCE Aequorea victoria  
ORGANISM Aequorea victoria  
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;  
Aequoreidae; Aequorea.  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
TITLE Novel low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: JP 2001506983-A 13 29-MAY-2001;  
BOSTON HEART FOUNDATION INC  
COMMENT PN JP 2001506983-A/13  
PD 29-MAY-2001  
PF 26-NOV-1997 JP 1998524870  
PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI  
ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
A6IK38/04, A6IK38/17, A6IK38/00, A6IK48/00, A6IK49/00, A6IK51/08, PC  
C07H21/00,  
PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC  
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CC Topology: Linear;  
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Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-976-740-22 (1-10) x BD056455 (1-30)  
QY 1 GIUASPASPProaspGlyPheleucly 10  
DB 1 GAGGATGATGACCCCGATGGCTCTTAGGC 30  
RESULT 6  
AR418294  
LOCUS AR418294 425 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 9791 from patent US 6639063.  
ACCESSION AR418294  
VERSION AR418294.1 GI:40173404  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.  
TITLE EST's and encoded human proteins  
JOURNAL Patent: US 6639063-A 9791 28-OCT-2003;  
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source Location/Qualifiers  
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Alignment Scores:  
Pred. No.: 0.136 Length: 425  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-976-740-22 (1-10) x BD056455 (1-30)

US-09-976-740-22 (1-10) x AR418294 (1-425)  
QY 1 GIUASPASPProaspGlyPheleucly 10  
DB 200 GAGGATGATGACCCCGATGGCTCTTAGGC 229  
RESULT 7  
BD113847  
LOCUS BD113847 425 bp DNA linear PAT 18-SEP-2002  
DEFINITION EST and encoded human protein.  
ACCESSION BD113847  
VERSION BD113847.1 GI:23208751  
KEYWORDS JP 2002010789-A/5924  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 425)  
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.  
TITLE EST and encoded human protein  
JOURNAL Patent: JP 2002010789-A 5924 15-JAN-2002;  
GENSET CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002010789-A/5924  
PD 15-JAN-2002  
PF 07-AUG-2000 JP 2000280989  
PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI  
GIORDANO  
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC  
C12N1/21,  
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC  
C12N15/00  
CC EST and encoded human protein  
FH Key Location/Qualifiers  
FT source 1..425  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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Alignment Scores:  
Pred. No.: 0.136 Length: 425  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-976-740-22 (1-10) x BD113847 (1-425)  
QY 1 GIUASPASPProaspGlyPheleucly 10  
DB 200 GAGGATGATGACCCCGATGGCTCTTAGGC 229  
RESULT 8  
BC007384  
LOCUS BC007384 982 bp mRNA linear PRI 16-SEP-2003  
DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone  
IMAGE:3677194), partial cds.  
ACCESSION BC007384  
VERSION BC007384.2 GI:33988219  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 982)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Teshigahara S., Carninci P., Prange C., Kana S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hui X., Gibbs R.A., Vellayon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez J., Whitting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G., Blakesley R.W., Touchman D.W., Green E.D., Dixon M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzyzinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

JOURNAL MEDLINE

22388257

12477932

2 (bases 1 to 982)

Strausberg, R.

Direct Submission

Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

On Aug 20, 2003 this sequence version replaced gi:13938477.

Contact: MGC help desk

Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

CDNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

Contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)

Anup Madan, Jessica Fahey, Erin Helton, Mark Kerteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>

Series: IRAL Plate: 24 Row: 9 Column: 10.

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3677194"

/tissue\_type="Lymph, Burkitt lymphoma"

/clone\_id="NIH MGC 8"

/lab\_host="DHIOB-R"

/note="Vector: pOTB7"

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/protein\_id="AAH07384.2"

/db\_xref="GI:3398820"

/db\_xref="LOCusID:90378"

/translation="PGAPAPASARPSKRGSEERVLKEEEDDDDEEDDDVSE GSEVPSDRPAGOHOLNGERQOSAKREYEWPCGPHOGQDSRGAPAGSGROY FEMAMNKEGCTASVATGPDSPVPLPGKALJGAGCTPGCGPGRKRPDPEVM TYMDVYETRTAGFPPEQATAFQEGEIDGSKLLIMORTVLTGLSLRLPALKITZHHI KYLQGHFEEDDDPDEFLG"

469..669

/gene="LOC90378"

/note="SAM; Region: Sterile alpha motif. Widespread domain

in signalling and nuclear proteins. In Eph-related tyrosine kinases, appears to mediate cell-cell initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"

/db\_xref="CDD:smart00454"

ORIGIN

Alignment Scores:

Pred. No.: 0.28 Length: 982

Score: 58.00 Matches: 10

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-976-740-22 (1-10) x BC007384 (1-982)

QY 1 GUAAPSAPSPProASPgiYPheLeuGly 10

DB 679 GAGGATGATGACCCGATGCTTCTTAGGC 708

RESULT 9

LOCUS BD275342 1134 bp DNA linear PAT 17-JUL-2003

DEFINITION 49 Human Secreted Proteins.

ACCESSION BD275342

VERSION BD275342.1 GI:33085110

KEYWORDS JP 2002539787-A/18.

SOURCE

ORGANISM Homo sapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1134)

AUTHORS Komatsoulis G., Rosen C.A. and Ruben S.M.

TITLE 49 Human Secreted Proteins

JOURNAL Patent: JP 2002539787-A 18 26-NOV-2002;

Human Genome Sciences Inc

OS Homo sapiens

PN JP 2002539787-A/18

PD 26-NOV-2002

PF 16-MAR-2000 JP 2000606742

PR 23-MAR-1999 US 60/126054, 10-DEC-1999 US 60/169916 PI

George Komatsoulis, craig a rosen, steven m ruben CC

FEATURES

Location/Qualifiers

1..1134

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 0.317 Length: 1134

Score: 58.00 Matches: 10

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-976-740-22 (1-10) x BD275342 (1-1134)

QY 1 GUAAPSAPSPProASPgiYPheLeuGly 10

DB 495 GAGGATGATGACCCGATGCTTCTTAGGC 466

RESULT 10

LOCUS ARI199535 1208 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 16 from patent US 6353451.

ACCESSION ARI199535

VERSION ARI199535.1 GI:20249609

KEYWORDS



SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1208)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 16 12-MAR-2002;  
FEATURES Location/Qualifiers  
source 1..1208  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.335 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AR199535 (1-1208)

QY 1 GIUASPAAPSPROASPGLYPHELEUGLY 10  
Db 622 GAGGATGATGACCCCGATGCTTCTTAGGC 651

RESULT 11  
LOCUS AR374687 1208 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 16 from patent US 6605588.  
ACCESSION AR374687  
VERSION AR374687.1 GI:40077502  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1208)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 16 12-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..1208  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.335 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AR374687 (1-1208)

QY 1 GIUASPAAPSPROASPGLYPHELEUGLY 10  
Db 622 GAGGATGATGACCCCGATGCTTCTTAGGC 651

RESULT 12  
LOCUS AR409322 1208 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 16 from patent US 6632923.  
ACCESSION AR409322  
VERSION AR409322.1 GI:40160110  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

SOURCE 1 (bases 1 to 1208)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 16 14-OCT-2003;  
FEATURES Location/Qualifiers  
source 1..1208  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.335 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AR409322 (1-1208)

QY 1 GIUASPAAPSPROASPGLYPHELEUGLY 10  
Db 622 GAGGATGATGACCCCGATGCTTCTTAGGC 651

RESULT 13  
LOCUS AX239573 1208 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 16 from Patent WO0164874.  
ACCESSION AX239573  
VERSION AX239573.1 GI:15797257  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in diagnosing  
and treating atherosclerosis  
JOURNAL Patent: WO 0164874-A 16 07-SEP-2001;  
Boston Heart Foundation, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..1208  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
<1..654  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC88296.1"  
/db\_xref="GI:15797258"  
/db\_xref="EMBL:NC088296"  
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GERGQSAKERKWTPCGPHQGDGEPAPGSGTRGVSTAAANKSGTASVATG  
DSPSPVPLPGPKPALPGADGTPFGCPGRKKEPSPVMTVDVVEYTEGFEPOAT  
AFQEOEIDKSHLMQRTDVLTLGSLIRGLPAKLYEHNIKYLQCGHFEDDDPDLGLG"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.335 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x AX239573 (1-1208)

QY 1 GIUASPAAPSPROASPGLYPHELEUGLY 10  
Db 622 GAGGATGATGACCCCGATGCTTCTTAGGC 651



misc\_feature

648..848  
/gene="LOC90378"  
/note="SAM; Region: Sterile alpha motif. Widespread domain in signalling and nuclear proteins. In Eph-related tyrosine kinases, appears to mediate cell-cell initiated signal transduction via the binding of SH2-containing proteins to a conserved tyrosine that is phosphorylated. In many cases mediates homodimerisation"  
/db\_xref="CDD:smart00454"

ORIGIN

Alignment Scores:

Pred. No.:	0.397	Length:	1470
Score:	58.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-22 (1-10) x BC030129 (1-1470)

QY	1		GluspaspaspProaspGlypHeLeuGly	10
DB	858	GAGGATGATGACCCGATGGCTTCTTAGGC		887

Search completed: March 13, 2004, 00:35:27  
Job time : 152.885 secs



GenCore version 5.1.6  
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OW protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:48:14 ; Search time 15.8507 Seconds

(without alignments)  
2680.137 Million cell updates/sec

Title: US-09-976-740-22

Perfect score: 58

Sequence: 1 EDDDDPDGFLG 10

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Pgapop 6.0 , Pgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 segs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n model -DEV=xlp  
-O=/cgnr\_1/USPRO\_pool\_p/US09976740/runatc\_10032004\_094547\_19532/app\_query\_faeta\_1.1898  
-DB=Geneseq\_29Jan04 -QMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0  
-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976740@cgnr\_1.1.1596 @runatc\_10032004\_094547\_19532 -NCPU=6 -ICPU=3  
-NO MAP -ARGSOUPTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=110 MARK TIMEOUT=30 THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_29Jan04:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	30	5	AAH26505
2	58	100.0	1134	2	AAC59574
3	58	100.0	1208	2	AAV32838
4	58	100.0	1208	5	AAH26494
5	58	100.0	1336	3	AAF21860
6	58	100.0	1614	5	AAH26499
7	58	100.0	12425	5	AAH26495
8	54	93.1	1362	5	AAH26489

9	54	93.1	1422	5	AAH26480	AAH26480	Rabbit 10
10	54	93.1	1617	2	AAV32835	AAV32835	Rabbit 10
11	54	93.1	1617	5	AAH26488	AAH26488	Rabbit 10
12	54	93.1	2561	5	AAH26500	AAH26500	Rabbit 10
13	44	75.9	539	7	ABX57356	ABX57356	Arabidops
14	44	75.9	2838	6	ABZ14501	ABZ14501	Arabidops
15	44	75.9	2838	7	ADA68111	ADA68111	Arabidops
16	44	75.9	3125	4	AAI66059	AAI66059	Arabidops
17	44	74.1	3250	4	AAIC0200	AAIC0200	Human sec
18	43	74.1	1455	6	ABL50160	ABL50160	Human wit
19	43	74.1	2415	4	ABL24639	ABL24639	Human wit
20	43	74.1	3590	7	ABZ36243	ABZ36243	Human sec
21	43	74.1	6647	4	ABL24638	ABL24638	Human sec
22	42	72.4	1936	3	AAA40319	AAA40319	S. olerac
23	41	70.7	404	7	ABX53231	ABX53231	Bovine ES
24	41	70.7	421	6	ABN75194	ABN75194	Human ORF
25	41	70.7	442	4	AAK88442	AAK88442	Human dig
26	41	70.7	442	5	AAK39543	AAK39543	CDNA enco
27	41	70.7	442	8	ADB32269	ADB32269	Human nov
28	41	70.7	1169	9	ADC30335	ADC30335	Human nov
29	41	70.7	1406	9	ADD30425	ADD30425	Plant yle
30	41	70.7	1406	9	ADB31450	ADB31450	Plant yle
31	41	70.7	1470	6	ABZ11247	ABZ11247	Human pol
32	41	70.7	1770	4	ABL05627	ABL05627	Drosophila
33	41	70.7	2000	7	ADA72766	ADA72766	Rice gene
34	41	70.7	2018	6	ABQ79395	ABQ79395	Gab2 enco
35	41	70.7	2855	4	ABL05496	ABL05496	Drosophila
36	41	70.7	3095	2	AAQ38525	AAQ38525	Human CEN
37	41	70.7	3132	7	ABK46187	ABK46187	CDNA enco
38	41	70.7	3132	7	ABU050452	ABU050452	Human CEN
39	41	70.7	5788	4	ABL05626	ABL05626	Drosophila
40	41	70.7	6045	4	AAH18244	AAH18244	Human CDN
41	41	70.7	11774	4	AAK90413	AAK90413	Human dig
42	41	70.7	11774	4	AAK69391	AAK69391	Human imm
43	41	70.7	11774	5	AAK39969	AAK39969	Genomic s
44	41	70.7	11774	8	ADB32929	ADB32929	Human nov
45	41	70.7	61557	4	AAK59521	AAK59521	Protoninb

ALIGNMENTS

RESULT 1  
AAH26505 standard; DNA; 30 BP.

ID	AAH26505	standard; DNA; 30 BP.
AC	AAH26505;	
DT	12-NOV-2001	(first entry)
DE	Low density lipoprotein binding protein (LBP) polynucleotide.	
XX		
XX	Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;	
KM	antiatherosclerotic; therapy; diagnosis; vaccine; ss.	
XX		
OS	Mammalia.	
XX		
PN	WO200164874-A2.	
PD	07-SEP-2001.	
XX		
PF	28-FEB-2001; 2001WO-US006356.	
XX		
PR	02-MAR-2000; 2000US-00517849.	
PR	14-JUL-2000; 2000US-00616289.	
XX		
PA	(BOST-) BOSTON HEART FOUND INC.	
PI	Lees AM, Lees RS, Law SM, Arjona AA;	
XX	WPI; 2001-565505/63.	
DR		
XX		
XX	New isolated low density lipoprotein binding polypeptide for treating,	
PT	diagnosing and/or identifying therapeutic agents for atherosclerosis.	

XX PS Disclosure; Page 9; 143pp; English.

XX CC The present sequence is that of a polynucleotide encoding a fragment of

XX CC novel low density lipoprotein binding proteins (LDLs) of the invention

XX CC (see AAB32797-820). LDLs are capable of binding to native and methylated

XX CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel

XX CC LDLs and their fragments are claimed, as well as expression vectors,

XX CC cells and methods of producing the LDLs. Methods of determining if an

XX CC animal is at risk for atherosclerosis, methods for evaluating a cell

XX CC having an abnormality in structure or metabolism of LDL are also claimed,

XX CC as are pharmaceutical compositions comprising an LDL polypeptide or

XX CC nucleic acid, and vaccine compositions

XX SQ Sequence 30 BP; 6 A; 7 C; 10 G; 7 T; 0 U; 0 Other;

XX Alignment Scores:

XX Pred. No.: 0.0025 Length: 30

XX Score: 58.00 Matches: 10

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: Gaps: 0

XX US-09-976-740-22 (1-10) x AAC26505 (1-30)

XX QY 1 GluAspAspAspProAspGlyPheLeuGly 10

XX Db 1 GAGGATGATGACCCCGATGCTTCTTAGGC 30

XX RESULT 2

XX AAC59574/C

XX ID AAC59574 standard; cDNA; 1134 BP.

XX AC AAC59574;

XX DT 26-JAN-2001 (first entry)

XX DE Human secreted protein gene 9 SEQ ID NO:19.

XX XX Human; secreted protein; diagnosis; neuroprotective; cytoskeletal;

XX KW cardiocactive; immunomodulatory; muscular active general; vulnary;

XX KW gastrointestinal; nephrotoxic; antinefactive; gynaeological;

XX KW and antibacterial; gene therapy; detection; cancer; chromosome marker;

XX KW chromosome identification; neural disorder; immune disorder;

XX KW muscular disorder; reproductive disorder; gastrointestinal disorder;

XX KW pulmonary disorder; cardiovascular disorder; renal disorder;

XX KW proliferative disorder; wound healing; infectious disease; preservative;

XX KW food additive; ss.

XX OS Homo sapiens.

XX XX W0200056883-A1.

XX XX 28-SEP-2000.

XX PF 16-MAR-2000; 2000WO-US006822.

XX XX 23-MAR-1999; 99US-0126054P.

XX PR 10-DEC-1999; 99US-0169916P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PA Rosen CA, Ruben SM, Komatsoulis G;

XX PI WPI, 2000-587666/55.

XX DR P-PSDB; AAB34307.

XX XX Human secreted proteins and gene sequences encoding them, useful for

XX PT detecting, preventing, and treating disorders such as cancer,

XX PT neurological disorders and immune system disorders.

PS Claim 1; Page 344; 429pp; English.

XX CC The polynucleotide sequences given in AAC59566 to AAC59614 encode the

XX CC human secreted proteins given in AAB34299 to AAB34347. AAB34348 to

XX CC AAB34437 represent human secreted polypeptide sequences and proteins

XX CC homologous to them, which are given in the exemplification of the present

XX CC invention. Human secreted proteins have activities based on the tissues

XX CC and cells the genes are expressed in. Example of activities include:

XX CC neuroprotective; cytoskeletal; cardiovascular; immunomodulatory; muscular

XX CC active general; vulnary; gastrointestinal; nephrotoxic; antinefactive;

XX CC gynaeological; and antibacterial. The polynucleotides can be used for

XX CC the detection of various disorders such as cancer, chromosome

XX CC identification, as chromosome markers, and for numerous other diagnostic

XX CC or research purposes. The secreted proteins can be used to treat

XX CC disorders such as neural, immune, muscular, reproductive,

XX CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative

XX CC disorders, wound healing, and infectious diseases. The proteins can also

XX CC be used as a food additive or preservative to increase or decrease

XX CC storage capabilities. AAC59557 to AAC59565 and AAB34298 represent

XX CC sequences used in the exemplification of the present invention

XX SQ Sequence 1134 BP; 248 A; 294 C; 366 G; 225 T; 0 U; 1 Other;

XX Alignment Scores:

XX Pred. No.: 0.133 Length: 1134

XX Score: 58.00 Matches: 10

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 100.00% Indels: 0

XX DB: Gaps: 0

XX US-09-976-740-22 (1-10) x AAC59574 (1-1134)

XX QY 1 GluAspAspAspProAspGlyPheLeuGly 10

XX Db 495 GAGGATGATGACCCCGATGCTTCTTAGGC 466

XX RESULT 3

XX AAV32838

XX ID AAV32838 standard; cDNA; 1208 BP.

XX AC AAV32838;

XX DT 09-NOV-1998 (first entry)

XX DE Human low density lipoprotein binding protein LBP-2 cDNA.

XX XX Human low density lipoprotein binding protein; LDL binding protein 2; LBP-2;

XX KW receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.

XX KW food additive; ss.

XX OS Homo sapiens.

XX XX Key

XX FH Location/Qualifiers

XX FT 1..654

XX CD CDS

XX FT /\*tag= a

XX FT 22..99

XX FT /\*tag= c

XX FT /\*note= "Claim 13"

XX FT 22..66

XX FT /\*tag= b

XX FT /\*note= "Claim 12"

XX FT 67..99

XX FT /\*tag= d

XX FT /\*note= "Claim 14"

XX FT 622..651

XX FT /\*tag= e

XX FT /\*note= "Claim 15"

XX XX W09823282-A1.

XX XX 04-JUN-1998.

XX XX 26-NOV-1997; 97WO-US021857.

XX 27-NOV-1996; 96US-0031930P.  
PR 03-JUN-1997; 97US-0048547P.  
XX  
PA (BOST-) BOSTON HEART FOUND INC.  
XX  
FI Lees AM, Lees RS, Law SW, Arizona AA;  
XX  
DR WPI; 1998-322455/28.  
XX P-PSDB; AAM49041.  
XX  
PT Nucleic acid encoding low density lipoprotein binding proteins and  
PT related vectors - transformed cells, proteins, and modulators of binding,  
PT useful for treatment and diagnosis of atherosclerosis and for identifying  
PT subjects at risk.  
XX  
PS Claim 9; Fig 16; 47pp; English.  
XX  
CC This cDNA clone codes for novel human low density lipoprotein (LDL)  
CC binding protein LBP-2 (see AAM49041). It was isolated by screening human  
CC liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA  
CC clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAM49037-  
CC 42) are claimed. An abnormality in LBP metabolism or structure is  
CC diagnostic of a risk for atherosclerosis. The invention provides: methods  
CC for determining if an animal is at risk for atherosclerosis (e.g. for  
CC prenatal screening); methods for treating atherosclerosis (including gene  
CC therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent  
CC formation of atherosclerotic plaques; and methods for treating a cell  
CC having an abnormality in LBP structure or metabolism. Pharmaceutical and  
CC vaccine compositions are also provided, as well as recombinant vectors  
CC and host cells used to produce recombinant LBP  
XX  
SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;  
XX  
Alignment Scores:  
Pred. No.: 0.143 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-09-976-740-22 (1-10) x AAV32838 (1-1208)  
QY 1 GUASPAAPSPProASPGlypHeuGLy 10  
Db 622 GAGGATGATGACCCCGATGCGCTTTAGGC 651  
RESULT 4  
AAH26494  
ID AAH26494 standard; cDNA; 1208 BP.  
XX  
AC AAH26494;  
XX  
DT 12-NOV-2001 (first entry)  
XX  
DE Human low density lipoprotein binding protein 2 (LBP-2) cDNA.  
XX  
KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
KW ss.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX FH Key Location/Qualifiers  
XX FT 1..654  
XX FT /\*tag= a  
XX FT /partial  
XX  
XX MO200164874-A2.  
XX  
XX PD 07-SEP-2001.

PF 28-FEB-2001; 2001WO-US006356.  
XX  
XX 02-MAR-2000; 2000US-00517849.  
PR 14-JUL-2000; 2000US-00616289.  
XX  
PA (BOST-) BOSTON HEART FOUND INC.  
XX  
FI Lees AM, Lees RS, Law SW, Arizona AA;  
XX  
DR WPI; 2001-565505/63.  
XX P-PSDB; AAB82803.  
XX  
PT New isolated low density lipoprotein binding polypeptide for treating,  
PT diagnosing and/or identifying therapeutic agents for atherosclerosis.  
XX  
XX Example 4; Fig 16; 143pp; English.  
XX  
CC The present sequence is that of a partial cDNA encoding novel human low  
CC density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were  
CC isolated from human foetal brain, liver and aorta cDNA libraries using  
CC rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in  
CC AAB8499, and a genomic DNA sequence is given in AAH26495. LBP-2 nucleic  
CC acids are among claimed polynucleotides of the invention that encode  
CC novel polypeptides capable of binding to native and methylated LDL. Also  
CC claimed are isolated LBP polypeptides, and biologically active fragments  
CC and analogues of them, as well as expression vectors, cells and methods  
CC of producing the LBPs. Methods of determining if an animal is at risk for  
CC atherosclerosis, methods for evaluating an agent for use in treating  
CC atherosclerosis, and methods for treating a cell having an abnormality in  
CC structure or metabolism of LBP are claimed. Pharmaceutical compositions  
CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions,  
CC are also claimed  
XX  
SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;  
XX  
Alignment Scores:  
Pred. No.: 0.143 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-09-976-740-22 (1-10) x AAH26494 (1-1208)  
QY 1 GUASPAAPSPProASPGlypHeuGLy 10  
Db 622 GAGGATGATGACCCCGATGCGCTTTAGGC 651  
RESULT 5  
AAF21860  
ID AAF21860 standard; DNA; 1336 BP.  
XX  
AC AAF21860;  
XX  
DT 27-MAR-2001 (first entry)  
XX  
DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.  
XX  
KW Human; breast cancer; ovarian cancer; cytosolic; immunosuppressive;  
KW neutropenic; neuroprotective; antiviral; antiinflammatory; hepatotropic;  
KW antidiabetic; antiinflammatory; antiviral; vulnerey; anticonvulsant;  
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KW cardiovascular disorder; wound healing; neurological disease; ds.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX FH Key Location/Qualifiers  
XX FT 1..1336  
XX FT /\*tag= a  
XX FT /partial  
XX  
XX MO200055173-A1.  
XX  
XX PD 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005881.  
XX 12-MAR-1999; 99US-0124270P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Ruben SM;  
XX WPI; 2000-611515/58.  
XX P-PSDB; AAB58957.  
XX  
XX New human breast and ovarian cancer associated gene sequences and the  
XX polypeptides encoded by these genes, useful in the prevention, treatment  
XX and diagnosis of cancer, immune disorders, cardiovascular disorders and  
XX neurological diseases.  
XX  
XX Claim 1; Page 670-671; 1299pp; English.  
XX  
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are  
XX associated with breast and ovarian cancer. Included in the invention are  
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
XX isolation and characterization of the DNA and protein sequences of the  
XX invention. The breast and ovarian cancer associated DNA, protein, agonist  
XX or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;  
XX neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;  
XX antiinflammatory; antitumor; anticonvulsant; antidiabetic;  
XX antitubercular; antiparasitic and cardiant activity. The polynucleotide and  
XX protein sequences are used in the diagnosis of cancer, particularly  
XX breast and ovarian cancer. The nucleic acid sequences, proteins, agonists  
XX and antagonists may also be used in the diagnosis, prevention and treatment  
XX of immune disorders e.g. Addison's disease, allergies, autoimmune  
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
XX cardiovascular disorders such as myocardial ischaemia; wound healing;  
XX neurological diseases such as cerebral anoxia and epilepsy; and  
XX infectious diseases  
XX  
XX SQ Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 0.159 Length: 1336  
XX Score: 58.00 Matches: 10  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 3 Gaps: 0  
XX  
XX US-09-976-740-22 (1-10) x AAF21860 (1-1336)  
XX  
XX QY 1 GluAspAspAspProAspGlyPheLeuGly 10  
XX DB 694 GAGGATGATGACCCCGATGCTTTAGGC 723  
XX  
XX RESULT 6  
XX AAH26499  
XX ID AAH26499 standard; DNA; 1614 BP.  
XX  
XX AC AAH26499;  
XX  
XX DT 12-NOV-2001 (first entry)  
XX  
XX DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.  
XX  
XX KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
XX atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
XX ds.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200164874-A2.  
XX

PD 07-SEP-2001.  
XX  
XX PF 28-FEB-2001; 2001WO-US006356.  
XX  
XX PR 02-MAR-2000; 2000US-00517849.  
XX 14-JUL-2000; 2000US-00616289.  
XX  
XX PA (BOST-) BOSTON HEART FOUND INC.  
XX  
XX PI Lees AM, Lees RS, Law SW, Arjona AA;  
XX WPI; 2001-565505/63.  
XX P-PSDB; AAB82806.  
XX  
XX PT New isolated low density lipoprotein binding polypeptide for treating,  
XX diagnosing and/or identifying therapeutic agents for atherosclerosis.  
XX  
XX PS Claim 7; Fig 7A; 143pp; English.  
XX  
XX The present sequence is that of the coding region of the human gene (see  
XX also AAH26499) encoding novel human low density lipoprotein binding  
XX protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA  
XX library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the  
XX present sequence differs from that predicted from a cDNA clone (see  
XX AAB82803) in that it contains an additional 321 amino acids at its N-  
XX terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among  
XX claimed polynucleotides of the invention that encode novel polypeptides  
XX capable of binding to native and methylated LDL. Also claimed are  
XX isolated LBP polypeptides, and biologically active fragments and  
XX analogues of them, as well as expression vectors, cells and methods of  
XX producing the LBPs. Methods of determining if an animal is at risk for  
XX atherosclerosis, methods for evaluating an agent for use in treating  
XX atherosclerosis, and methods for treating a cell having an abnormality in  
XX structure or metabolism or LBP are claimed. Pharmaceutical compositions  
XX comprising an LBP polypeptide or nucleic acid, and vaccine compositions,  
XX are also claimed  
XX  
XX SQ Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 0.196 Length: 1614  
XX Score: 58.00 Matches: 10  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 5 Gaps: 0  
XX  
XX US-09-976-740-22 (1-10) x AAH26499 (1-1614)  
XX  
XX QY 1 GluAspAspAspProAspGlyPheLeuGly 10  
XX DB 1585 GAGGATGATGACCCCGATGCTTTAGGC 1614  
XX  
XX RESULT 7  
XX AAH26499  
XX ID AAH26499 standard; DNA; 12425 BP.  
XX  
XX AC AAH26499;  
XX  
XX DT 12-NOV-2001 (first entry)  
XX  
XX DE Human low density lipoprotein binding protein 2 (LBP-2) gene.  
XX  
XX KW Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
XX atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
XX ds.  
XX  
XX OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT CDS 2832..5153  
XX FT /\*tag= a  
XX FT /note= "includes introns"  
XX



```

FT exon 2832..3785
FT intron /*cag= b
FT intron 3786..4207
FT exon /*cag= c
FT exon 4208..4502
FT intron /*cag= d
FT intron 4503..4593
FT exon /*cag= e
FT intron 4594..4694
FT intron /*cag= f
FT intron 4695..4787
FT exon /*cag= g
FT exon 4788..4899
FT intron /*cag= h
FT intron 4900..4994
FT exon /*cag= i
FT exon 4995..5153
FT exon /*cag= j

W0200164874-A2.
XX
XX PD 07-SEP-2001.
XX
XX PF 28-FEB-2001; 2001WO-US006356.
XX
XX PR 02-MAR-2000; 2000US-00517849.
XX PR 14-JUL-2000; 2000US-00616289.
XX
XX PA (BOST-) BOSTON HEART FOUND INC.
XX
XX PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
XX DR WPI; 2001-565505/63.
XX DR P-PSDB; AAB82799.
XX
XX PT New isolated low density lipoprotein binding polypeptide for treating,
XX diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
XX PS Example 4; Fig 23; 143pp; English.
XX
XX CC The present sequence is that of genomic DNA encoding novel human low
XX density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was
XX isolated from a human genomic library by screening with LBP-2 cDNA (see
XX AAB26494). The open reading frame spans 5 exons. Human LBP-2 nucleic
XX acids are among claimed polynucleotides of the invention that encode
XX novel polypeptides, termed LBPs, capable of binding to native and
XX methylated LDL. Also claimed are isolated LBP polypeptides, and
XX biologically active fragments and analogues of them, as well as
XX expression vectors, cells and methods of producing the LBPs. Methods of
XX determining if an animal is at risk for atherosclerosis, methods for
XX evaluating an agent for use in treating atherosclerosis, and methods for
XX treating a cell having an abnormality in structure or metabolism of LBP
XX are claimed. Pharmaceutical compositions comprising an LBP polypeptide or
XX nucleic acid, and vaccine compositions, are also claimed.
XX
SQ Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;

```

```

ID AAB26489 standard; cDNA; 1362 BP.
XX
XX AC AAB26489;
XX
XX DT 12-NOV-2001 (first entry)
XX
XX DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.
XX
XX KW Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;
XX atherosclerosis; antiatherosclerotic; gene therapy; diagnosis; vaccine;
XX ss.
XX
XX OS Oryctolagus cuniculus.
XX
XX FH Key Location/Qualifiers
FT CDS 1..955
FT FT /*cag= a
FT FT /partial
XX
XX PN W0200164874-A2.
XX
XX PD 07-SEP-2001.
XX
XX PF 28-FEB-2001; 2001WO-US006356.
XX
XX PR 02-MAR-2000; 2000US-00517849.
XX PR 14-JUL-2000; 2000US-00616289.
XX
XX PA (BOST-) BOSTON HEART FOUND INC.
XX
XX PI Lees AM, Lees RS, Law SW, Arjona AA;
XX
XX DR WPI; 2001-565505/63.
XX DR P-PSDB; AAB82799.
XX
XX PT New isolated low density lipoprotein binding polypeptide for treating,
XX diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX
XX PS Example 2; Fig 12; 143pp; English.
XX
XX CC The present sequence is that of cDNA encoding a portion (see AAB82799) of
XX novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA
XX was isolated following screening of a rabbit cDNA library for clones
XX encoding LBPs that bound to both native low density lipoprotein (LDL) and
XX methyl LDL. A full-length sequence for LBP-2 is given in AAB26500. The
XX invention provides claimed polynucleotides encoding novel polypeptides
XX which are capable of binding to native and methylated LDL, the isolated
XX polypeptides, termed LBPs, and biologically active fragments and
XX analogues of them, as well as expression vectors, cells and methods of
XX producing the LBPs. Also claimed are methods of determining if an animal
XX is at risk for atherosclerosis, methods for evaluating an agent for use
XX in treating atherosclerosis, and methods for treating a cell having an
XX abnormality in structure or metabolism of LBP. Pharmaceutical
XX compositions comprising an LBP polypeptide or nucleic acid, and vaccine
XX compositions, are also claimed.
XX
SQ Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 1.82 Length: 12425
Score: 58.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-09-976-740-22 (1-10) x AAB26495 (1-12425)
OY 1 GIUASPAAPAPPCoaspGlyPheLeuGly 10
Db 5121 GAGGATGATGACCCCGATGCTTCTTAGGC 5150

```

```

Alignment Scores:
Pred. No.: 0.941 Length: 1362
Score: 54.00 Matches: 9
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 90.00% Mismatches: 0
Query Match: 93.10% Indels: 0
DB: 5 Gaps: 0
US-09-976-740-22 (1-10) x AAB26489 (1-1362)
OY 1 GIUASPAAPAPPCoaspGlyPheLeuGly 10
Db 667 GAGGAGATGACCCCGAGAGCTTCTTGGA 696

```



CC therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent  
CC formation of atherosclerotic plaque; and methods for treating a cell  
CC having an abnormality in LBP structure or metabolism. Pharmaceutical and  
CC vaccine compositions are also provided, as well as recombinant vectors  
CC and host cells used to produce recombinant LBP

XX Sequence 1617 BP; 290 A; 513 C; 529 G; 285 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.14	Length:	1617
Score:	54.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	90.00%	Mismatches:	0
Query Match:	93.10%	Indels:	0
DB:	2	Gaps:	0

US-09-976-740-22 (1-10) x AAH26488 (1-1617)

QY 1 GluAspAspAspProAspGlyPheLeuGly 10

DB 922 GAGGACGATGACCCGGAAGGCTTCTGCGA 951

RESULT 11

AAH26488  
ID AAH26488 standard; cDNA, 1617 BP.

AC AAH26488;

DT 12-NOV-2001 (first entry)

XX Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.

XX Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;

XX atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

FT CDS 1..955

FT /\*tag= a

FT /partial

FT /note= "includes in-frame stop codon at nucleotides

XX 28..30"

XX WO200164874-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006356.

XX 02-MAR-2000; 2000US-00517849.

XX 14-JUL-2000; 2000US-00616289.

XX (BOST-) BOSTON HEART FOUND INC.

XX Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 2001-565505/63.

XX P-PSDB; AAB82798.

XX New isolated low density lipoprotein binding polypeptide for treating,

XX diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX Example 2; Fig 11; 143pp; English.

CC polypeptides, termed LBPs, and biologically active fragments and  
CC analogues of them, as well as expression vectors, cells and methods of  
CC producing the LBPs. Also claimed are methods of determining if an animal  
CC is at risk for atherosclerosis, methods for evaluating an agent for use  
CC in treating atherosclerosis, and methods for treating a cell having an  
CC abnormality in structure or metabolism of LBP. Pharmaceutical  
CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine  
CC compositions, are also claimed

XX Sequence 1617 BP; 289 A; 513 C; 530 G; 285 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.14	Length:	1617
Score:	54.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	90.00%	Mismatches:	0
Query Match:	93.10%	Indels:	0
DB:	5	Gaps:	0

US-09-976-740-22 (1-10) x AAH26488 (1-1617)

QY 1 GluAspAspAspProAspGlyPheLeuGly 10

DB 922 GAGGACGATGACCCGGAAGGCTTCTGCGA 951

RESULT 12

AAH26500  
ID AAH26500 standard; cDNA; 2561 BP.

AC AAH26500;

DT 12-NOV-2001 (first entry)

XX Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.

XX Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;

XX atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

FT CDS 246..1928

FT /\*tag= a

XX WO200164874-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006356.

XX 02-MAR-2000; 2000US-00517849.

XX 14-JUL-2000; 2000US-00616289.

XX (BOST-) BOSTON HEART FOUND INC.

XX Lees AM, Lees RS, Law SW, Arjona AA;

XX WPI; 2001-565505/63.

XX P-PSDB; AAB82807.

XX New isolated low density lipoprotein binding polypeptide for treating,

XX diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX Claim 4; Fig 2A; 143pp; English.

XX The present sequence is that of cDNA encoding novel rabbit low density  
XX lipoprotein binding protein 1 (LBP-2, see AAB82807). The cDNA was  
XX isolated following screening of a rabbit cDNA library for clones encoding  
XX LBPs that bound to both native low density lipoprotein (LDL) and methyl  
XX LDL. The invention provides claimed polynucleotides encoding novel  
XX polypeptides which are capable of binding to native and methylated LDL,  
XX the isolated polypeptides, termed LBPs, and biologically active fragments

CC and analogues of them, as well as expression vectors, cells and methods  
CC of producing the LBPs. Also claimed are methods of determining if an  
CC animal is at risk for atherosclerosis, methods for evaluating an agent  
CC for use in treating atherosclerosis, and methods for treating a cell  
CC having an abnormality in structure or metabolism of LBP. Pharmaceutical  
CC compositions comprising an LBP polypeptide or nucleic acid, and vaccine  
CC compositions, are also claimed

XX  
SQ Sequence 2561 BP, 372 A, 937 C, 879 G, 373 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1.88	Length:	2561
Score:	54.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	90.00%	Mismatches:	0
Query Match:	93.10%	Indels:	0
DB:	5	Gaps:	0

US-09-976-740-22 (1-10) x AAH26500 (1-2561)

Qy 1 GluaspaspapPrcaspGlyPheleugly 10  
|||||  
Db 1866 GAGAGCAGTACCCCGAAGCCTTCCTGGGA 1895

RESULT 13

ID ABX57356 standard; DNA, 539 BP.

XX  
AC ABX57356;

XX  
DT 20-FEB-2003 (first entry)

XX  
DE Arabidopsis thaliana polynucleotide #708.

XX  
KW Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;  
KW genetic modification; environmental stress; disease resistance;  
KW fungicide; insecticide; stress tolerance.

XX  
OS Arabidopsis thaliana.

XX  
PN US2002040489-A1.

XX  
PD 04-APR-2002.

XX  
PF 26-JAN-2001; 2001US-00770152.

XX  
PR 27-JAN-2000; 2000US-0178503P.

XX  
PA (GORL/) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAM/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHEW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRICK/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HUREBAN P.

XX  
PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;  
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;  
PI Hurban P;  
XX

DR WPI, 2003-110410/10.

XX  
PT Novel Arabidopsis thaliana nucleic acid useful for identifying homologous  
PT or related genes, and to create genetically modified and transgenic  
PT organisms, such as plant cells and plants.

XX  
PS Claim 1; SEQ ID NO 708; 45pp; English.

XX  
CC The invention relates to Arabidopsis thaliana nucleic acid sequences. The  
CC DNA sequences and the polypeptides they encode are useful for identifying  
CC homologous or related genes, for producing compositions that modulate the  
CC expression or function of the polypeptide, for mapping functional  
CC regions of the protein, in diagnosis, for studying associated  
CC physiological pathways, for genetic manipulation of cells, preferably  
CC plant cells, in screening assays of various plant strains to determine  
CC the strains that are capable of withstanding a particular disease or  
CC environmental stress, for enhancing or inhibiting production of  
CC biosynthetic products in plants and to create genetically modified and  
CC transgenic organisms, such as plant cells and plants. Transgenic plants  
CC are useful for introducing or improving disease resistance and stress  
CC tolerance in plants, screening biologically active agents, such as  
CC fungicides and insecticides, and for elucidating biochemical pathways.  
CC Sequences ABX56649-ABX57647 represent Arabidopsis thaliana  
CC polynucleotides of the invention. Note: The sequence data for this patent  
CC did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX  
SQ Sequence 539 BP, 130 A, 151 C, 100 G, 158 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	27.5	Length:	539
Score:	44.00	Matches:	8
Percent Similarity:	80.00%	Conservative:	0
Best Local Similarity:	80.00%	Mismatches:	2
Query Match:	75.86%	Indels:	0
DB:	7	Gaps:	0

US-09-976-740-22 (1-10) x ABX57356 (1-539)

Qy 1 GluaspaspapPrcaspGlyPheleugly 10  
|||||  
Db 355 GAGATCGTATCCTCAAGGCTTCCTTGA 384

RESULT 14

ID ABZ14501 standard; DNA, 2838 BP.

XX  
AC ABZ14501;

XX  
DT 21-JAN-2003 (first entry)

XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2306.

XX  
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX  
OS Arabidopsis thaliana.

XX  
PN WO200216655-A2.

XX  
PD 28-FEB-2002.

XX  
PF 24-AUG-2001; 2001WO-US026685.

XX  
PR 24-AUG-2000; 2000US-0227866P.

XX  
PR 26-JAN-2001; 2001US-0264647P.

XX  
PR 22-JUN-2001; 2001US-0300111P.

XX  
PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PA (HARP ) HARPER JF, Kreps J, Wang X, Zhu T;  
PI Harper JF, Kreps J, Wang X, Zhu T;  
XX  
XX WPI, 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
XX  
XX Claim 144; SEQ ID NO 2306; 577pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (AB212196/AB217574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 2838 BP; 784 A; 600 C; 703 G; 751 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 169 Length: 2838  
Score: 44.00 Matches: 8  
Percent Similarity: 80.00% Conservative: 0  
Best Local Similarity: 80.00% Mismatches: 2  
Query Match: 75.86% Indels: 0  
DB: Gaps: 0  
US-09-976-740-22 (1-10) x AB214501 (1-2838)  
QY 1 GUUASPASPProAspGlyPheLeuGly 10  
DB 352 GAGGATCGTATCCTCAAGCTTCTTGA 381  
RESULT 15  
ADA68111  
ID ADA68111 standard; DNA; 2838 BP.  
XX  
AC ADA68111;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Arabidopsis thaliana gene, SEQ ID 374.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200300898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,  
PI Karagiri F, Qian S, Tao Y, Whittham S, Xie Z, Zhu T, Zou G;  
XX  
DR WPI; 2003-175290/17.  
XX  
PT Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
PS Claim 6; SEQ ID NO 374; 899pp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 2838 BP; 784 A; 600 C; 703 G; 751 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 169 Length: 2838  
Score: 44.00 Matches: 8  
Percent Similarity: 80.00% Conservative: 0  
Best Local Similarity: 80.00% Mismatches: 2  
Query Match: 75.86% Indels: 0  
DB: Gaps: 0  
US-09-976-740-22 (1-10) x ADA68111 (1-2838)  
QY 1 GUUASPASPProAspGlyPheLeuGly 10  
DB 352 GAGGATCGTATCCTCAAGCTTCTTGA 381  
Search completed: March 12, 2004, 21:08:47  
Job time: 21.8507 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: March 12, 2004, 20:05:17 : Search time 3.39045 Seconds  
(without alignments)  
1636.805 Million cell updates/sec

Title: US-09-976-740-22  
Perfect score: 58  
Sequence: 1 EDDPDGFLG 10

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus.p2n.model -DEV=x1p  
-Q=/cgn2\_1/USPRO.spool/p/US09976740/runat.10032004.094549.19564/app.query.fasta\_1.1898  
-DB=Issued Patents NA -QMT=faesap -SUFFIX=rni -MINMATCH=0.1 -LOOPCT=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09976740 -CGN1\_1\_1235=runat.10032004.094549.19564 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	30	4	US-08-979-608A-33
2	58	100.0	30	4	US-09-517-849-33
3	58	100.0	30	4	US-09-616-289-33
4	58	100.0	425	4	US-09-621-976-9791
5	58	100.0	1208	4	US-08-979-608A-16
6	58	100.0	1208	4	US-08-517-849-16
7	58	100.0	1208	4	US-09-616-289-16
8	58	100.0	1614	4	US-09-616-289-45
9	58	100.0	12425	4	US-09-616-289-50
10	54	93.1	1362	4	US-08-979-608A-12
11	54	93.1	1362	4	US-09-517-849-12
12	54	93.1	1362	4	US-09-616-289-12

13	54	93.1	1422	4	US-08-979-608A-13	Sequence 13, Appl
14	54	93.1	1422	4	US-09-517-849-13	Sequence 13, Appl
15	54	93.1	1422	4	US-09-616-289-13	Sequence 13, Appl
16	54	93.1	1617	4	US-08-979-608A-11	Sequence 11, Appl
17	54	93.1	1617	4	US-09-517-849-11	Sequence 11, Appl
18	54	93.1	1617	4	US-09-616-289-11	Sequence 11, Appl
19	54	93.1	2561	4	US-09-616-289-48	Sequence 48, Appl
20	41	70.7	486	4	US-09-621-976-3195	Sequence 3195, Ap
21	41	70.7	2043	4	US-09-614-912-171	Sequence 171, Ap
22	40	69.0	1656	4	US-09-252-991A-8924	Sequence 8924, Ap
23	39	67.2	11282	4	US-09-754-250-3	Sequence 3, Appl
24	38	65.5	5410	4	US-09-221-017B-70	Sequence 70, Appl
25	37	63.8	642	4	US-08-956-171B-614	Sequence 614, Ap
26	37	63.8	648	4	US-09-228-986-26	Sequence 26, Appl
27	37	63.8	699	4	US-09-252-991A-575	Sequence 575, Ap
28	37	63.8	900	4	US-09-589-927-7	Sequence 7, Appl
29	37	63.8	900	4	US-09-277-665-7	Sequence 7, Appl
30	37	63.8	900	4	US-09-589-987-7	Sequence 7, Appl
31	37	63.8	1269	4	US-09-489-039A-979	Sequence 979, Ap
32	37	63.8	1368	2	US-08-738-172-3	Sequence 3, Appl
33	37	63.8	1416	4	US-09-711-164-273	Sequence 273, Ap
34	37	63.8	1425	4	US-09-489-039A-1173	Sequence 1173, Ap
35	37	63.8	1434	4	US-09-252-991A-522	Sequence 522, Ap
36	37	63.8	1458	4	US-09-252-991A-599	Sequence 599, Ap
37	37	63.8	2936	2	US-08-738-172-1	Sequence 2, Appl
38	37	63.8	4454	4	US-08-738-172-2	Sequence 2, Appl
39	36	62.1	284	4	US-09-016-434-416	Sequence 416, Ap
40	36	62.1	297	4	US-09-252-991A-8030	Sequence 8030, Ap
41	36	62.1	357	4	US-09-894-854-102	Sequence 102, Ap
42	36	62.1	477	4	US-09-446-754-7	Sequence 7, Appl
43	36	62.1	507	4	US-09-252-991A-14417	Sequence 14417, A
44	36	62.1	606	4	US-09-252-991A-3463	Sequence 3463, Ap
45	36	62.1	891	4	US-09-252-991A-8283	Sequence 8283, Ap

## ALIGNMENTS

RESULT 1  
US-08-979-608A-33  
Sequence 33, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

Law, Robert S.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson P.C.

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979 608A

FILING DATE: 26-NOV-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/048,547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031,530

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...30  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-08-979-608A-33  
Alignment Scores:  
Pred. No.: 0.000437 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-09-976-740-22 (1-10) x US-08-979-608A-33 (1-30)  
QY 1 GluspaaspProaspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30  
RESULT 2  
US-09-517-849-33  
Sequence 33, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2894  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...30  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-517-849-33  
Alignment Scores:  
Pred. No.: 0.000437 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-09-976-740-22 (1-10) x US-09-517-849-33 (1-30)  
QY 1 GluspaaspProaspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30  
RESULT 3  
US-09-616-289-33  
Sequence 33, Application US/09616289  
Patent No. 6632823  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,920  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
TYPE: DNA  
LENGTH: 30  
ORGANISM: Homo sapiens  
US-09-616-289-33  
Alignment Scores:  
Pred. No.: 0.000437 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-09-976-740-22 (1-10) x US-09-616-289-33 (1-30)  
QY 1 GluspaaspProaspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGGCTTCTTAGGC 30  
RESULT 4  
US-09-621-976-9791  
Sequence 9791, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
Cobert, S.



APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTS and Encoded Human Proteins.  
FILE REFERENCE: GENSET 054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 9791  
LENGTH: 425  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-621-976-9791

Alignment Scores:  
Pred. No.: 0.00805 Length: 425  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-976-740-22 (1-10) x US-09-621-976-9791 (1-425)

QY 1 GIUASPAPSPProAspGlyPheLeuGly 10  
Db 200 GAGGATGATGACCCCGATGCTTCTTAGGC 229

RESULT 5  
US-08-979-608A-16  
Sequence 16, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-Mar-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-08-979-608A-16

Alignment Scores:  
Pred. No.: 0.0254 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-976-740-22 (1-10) x US-08-979-608A-16 (1-1208)

QY 1 GIUASPAPSPProAspGlyPheLeuGly 10  
Db 622 GAGGATGATGACCCCGATGCTTCTTAGGC 651

RESULT 6  
US-09-517-849-16  
Sequence 16, Application US/09517849  
Patent No. 6605388  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-517-849-16

Alignment Scores:  
Pred. No.: 0.0254 Length: 1208  
Score: 58.00 Matches: 10

Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Conservative: 0  
Matches: 0  
Indels: 0  
Gaps: 0

US-09-976-740-22 (1-10) x US-09-517-849-16 (1-1208)

Qy 1 Gluaspaspaprcaspiglypneugly 10  
Db 622 GAGATGATGACCCCGATGGCTTCTTAGGC 651

RESULT 7

US-09-616-289-16  
Sequence 16, Application US/09616289  
Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 16  
LENGTH: 1208

TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)

US-09-616-289-16

Alignment Scores:

Pred. No.: 0.0254 Length: 1208  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

DB: 4

US-09-976-740-22 (1-10) x US-09-616-289-16 (1-1208)

Qy 1 Gluaspaspaprcaspiglypneugly 10  
Db 622 GAGATGATGACCCCGATGGCTTCTTAGGC 651

RESULT 8  
US-09-616-289-45

Sequence 45, Application US/09616289  
Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 45  
LENGTH: 1614

TYPE: DNA  
ORGANISM: Homo sapiens

FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1614)

US-09-616-289-45

Alignment Scores:

Pred. No.: 0.0349 Length: 1614  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

DB: 4

US-09-976-740-22 (1-10) x US-09-616-289-45 (1-1614)

Qy 1 Gluaspaspaprcaspiglypneugly 10  
Db 1585 GAGATGATGACCCCGATGGCTTCTTAGGC 1614

RESULT 9  
US-09-616-289-50

Sequence 50, Application US/09616289  
Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27

PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03

NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 50  
LENGTH: 12425

TYPE: DNA  
ORGANISM: Homo sapiens

US-09-616-289-50

Alignment Scores:

Pred. No.: 0.33 Length: 12425  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00%  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

DB: 4

US-09-976-740-22 (1-10) x US-09-616-289-50 (1-12425)

QY 1 Gluaspaspappproaspglypheleugly 10

Db 5121 GAGGATGATGACCCGAGAGGCTTCTTGGA 5150

RESULT 10

US-08-979-608A-12

Sequence 12, Application US/08979608A

Patent No. 6353451

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

Lees, Robert S.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979, 608A

FILING DATE: 26-Nov-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/948, 547

FILING DATE: 03-JUN-1997

APPLICATION NUMBER: US 60/031, 930

FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3593/59818)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1362 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...696

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-08-979-608A-12

Alignment Scores:

Pred. No.: 0.17 Length: 1362

Score: 54.00 Matches: 9

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 90.00% Mismatches: 0

Query Match: 93.10% Indels: 0

DB: 4 Gaps: 0

US-09-976-740-22 (1-10) x US-08-979-608A-12 (1-1362)

QY 1 Gluaspaspappproaspglypheleugly 10

Db 667 GAGGATGATGACCCGAGAGGCTTCTTGGA 696

RESULT 11

US-09-976-740-22 (1-10) x US-09-517-849-12 (1-1362)

QY 1 Gluaspaspappproaspglypheleugly 10

Db 667 GAGGATGATGACCCGAGAGGCTTCTTGGA 696

RESULT 11

US-09-976-740-22 (1-10) x US-09-517-849-12 (1-1362)

QY 1 Gluaspaspappproaspglypheleugly 10

Db 667 GAGGATGATGACCCGAGAGGCTTCTTGGA 696

RESULT 11

US-09-517-849-12

Sequence 12, Application US/09517849

Patent No. 6605588

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

Lees, Robert S.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/517, 849

FILING DATE: 02-Mar-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979, 608

FILING DATE: 26-Nov-1997

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1362 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...696

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-517-849-12

Alignment Scores:

Pred. No.: 0.17 Length: 1362

Score: 54.00 Matches: 9

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 90.00% Mismatches: 0

Query Match: 93.10% Indels: 0

DB: 4 Gaps: 0

US-09-976-740-22 (1-10) x US-09-517-849-12 (1-1362)

QY 1 Gluaspaspappproaspglypheleugly 10

Db 667 GAGGATGATGACCCGAGAGGCTTCTTGGA 696

RESULT 12

US-09-616-289-12

Sequence 12, Application US/09616289

Patent No. 6632923

GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

Lees, Robert S.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

PROTEINS AND THEIR USES IN DIAGNOSING AND

TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 1362  
TYPE: DNA  
ORGANISM: Oryctolagus cuniculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(696)  
US-09-616-289-12

Alignment Scores:  
Pred. No.: 0.17 Length: 1362  
Score: 54.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 90.00% Mismatches: 0  
Query Match: 93.10% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-22 (1-10) x US-09-616-289-12 (1-1362)

QY 1 Gluaspaspappproaspiglyphenleugly 10  
DB 667 GAGGACGATGACCCGGAAGGCTTCCTGGGA 696

RESULT 13  
US-08-879-608A-13  
Sequence 13, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-Nov-6355451-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis

REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1422 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...756  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-08-979-608A-13

Alignment Scores:  
Pred. No.: 0.178 Length: 1422  
Score: 54.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 90.00% Mismatches: 0  
Query Match: 93.10% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-22 (1-10) x US-08-979-608A-13 (1-1422)

QY 1 Gluaspaspappproaspiglyphenleugly 10  
DB 727 GAGGACGATGACCCGGAAGGCTTCCTGGGA 756

RESULT 14  
US-08-517-849-13  
Sequence 13, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1422 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...756  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-517-849-13

Alignment Scores:  
Pred. No.: 0.178 Length: 1422  
Score: 54.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 90.00% Mismatches: 0  
Query Match: 93.10% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-22 (1-10) x US-09-517-849-13 (1-1422)

Oy 1 GluAspAspAspProAspGlyPheLeuGly 10  
Db 727 GAGGACGATGACCCGGAAGGCTTCTCGGA 756

RESULT 15  
US-09-616-289-13  
Sequence 13, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 1422  
TYPE: DNA  
ORGANISM: Oryctolagus cuniculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(756)  
US-09-616-289-13

Alignment Scores:  
Pred. No.: 0.178 Length: 1422  
Score: 54.00 Matches: 9  
Percent Similarity: 100.00% Conservative: 1  
Best Local Similarity: 90.00% Mismatches: 0  
Query Match: 93.10% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-22 (1-10) x US-09-616-289-13 (1-1422)

Oy 1 GluAspAspAspProAspGlyPheLeuGly 10  
Db 727 GAGGACGATGACCCGGAAGGCTTCTCGGA 756



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 20:46:42 ; Search time 14.4676 Seconds  
(without alignments)  
254.725 Million cell updates/sec

Title: US-09-976-740-22  
Perfect score: 58  
Sequence: 1 EDDDDPGLG 10

Scoring table: BIOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.spool.p/US09976740/runat.10032004.094549.19588/app.query.fasta\_1.1898  
-DB=Published Applications NA -CMT=fastp -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCU=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blonsum62  
-TRANS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09976740 @CGN.1.1.712 @runat.10032004.094549.19588  
-NCPU=6 -ICPU=3 -NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications\_NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	58	100.0	30	9	US-09-962-055-33	Sequence 33, Appl
2	58	100.0	30	12	US-10-671-242-33	Sequence 33, Appl
3	58	100.0	30	13	US-10-023-529-33	Sequence 33, Appl
4	58	100.0	30	13	US-10-023-529-33	Sequence 33, Appl
5	58	100.0	30	15	US-10-616-187-33	Sequence 33, Appl
6	58	100.0	30	15	US-09-962-055-16	Sequence 16, Appl
7	58	100.0	1208	9	US-09-976-740-16	Sequence 16, Appl
8	58	100.0	1208	12	US-10-671-242-16	Sequence 16, Appl
9	58	100.0	1208	13	US-10-023-529-16	Sequence 16, Appl
10	58	100.0	1208	13	US-10-023-529-16	Sequence 16, Appl
11	58	100.0	1208	13	US-10-023-529-16	Sequence 16, Appl
12	58	100.0	1208	15	US-10-616-187-16	Sequence 16, Appl
13	58	100.0	1336	14	US-10-102-806-247	Sequence 247, App
14	58	100.0	1445	10	US-09-945-527-6	Sequence 6, Appl
15	58	100.0	1614	9	US-09-976-740-45	Sequence 45, Appl
16	58	100.0	1614	12	US-10-671-242-45	Sequence 45, Appl
17	58	100.0	1614	13	US-10-023-529-45	Sequence 45, Appl
18	58	100.0	1614	13	US-10-023-529-45	Sequence 45, Appl
19	58	100.0	1614	15	US-10-616-187-45	Sequence 45, Appl
20	58	100.0	12425	9	US-09-976-740-50	Sequence 50, Appl
21	58	100.0	12425	12	US-10-671-242-50	Sequence 50, Appl
22	58	100.0	12425	13	US-10-023-529-50	Sequence 50, Appl
23	58	100.0	12425	13	US-10-023-529-50	Sequence 50, Appl
24	58	100.0	12425	15	US-10-616-187-50	Sequence 50, Appl
25	54	93.1	1362	9	US-09-962-055-12	Sequence 12, Appl
26	54	93.1	1362	9	US-09-976-740-12	Sequence 12, Appl
27	54	93.1	1362	12	US-10-671-242-12	Sequence 12, Appl
28	54	93.1	1362	13	US-10-023-529-12	Sequence 12, Appl
29	54	93.1	1362	13	US-10-023-529-12	Sequence 12, Appl
30	54	93.1	1362	15	US-10-616-187-12	Sequence 12, Appl
31	54	93.1	1422	9	US-09-962-055-13	Sequence 13, Appl
32	54	93.1	1422	9	US-09-976-740-13	Sequence 13, Appl
33	54	93.1	1422	12	US-10-671-242-13	Sequence 13, Appl
34	54	93.1	1422	13	US-10-023-529-13	Sequence 13, Appl
35	54	93.1	1422	13	US-10-023-529-13	Sequence 13, Appl
36	54	93.1	1422	15	US-10-616-187-13	Sequence 13, Appl
37	54	93.1	1617	9	US-09-962-055-11	Sequence 11, Appl
38	54	93.1	1617	9	US-09-976-740-11	Sequence 11, Appl
39	54	93.1	1617	12	US-10-671-242-11	Sequence 11, Appl
40	54	93.1	1617	13	US-10-023-529-11	Sequence 11, Appl
41	54	93.1	1617	13	US-10-023-529-11	Sequence 11, Appl
42	54	93.1	1617	15	US-10-616-187-11	Sequence 11, Appl
43	54	93.1	2561	9	US-09-976-740-48	Sequence 48, Appl
44	54	93.1	2561	12	US-10-671-242-48	Sequence 48, Appl
45	54	93.1	2561	13	US-10-023-529-48	Sequence 48, Appl

## ALIGNMENTS

RESULT 1  
US-09-962-055-33  
Sequence 33, Application US/09962055  
Patent No. US20020052039A1  
GENERAL INFORMATION:  
APPLICANT: lees, Ann M.  
Law, Simon W.  
Aljona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA: US/09/962,055  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/55818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..30  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-962-055-33  
Alignment Scores:  
Pred. No.: 0.00149 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-976-740-22 (1-10) x US-09-962-055-33 (1-30)  
QY 1 GlusapaspapProaspGlypheLeuGly 10  
Db 1 GAGGATGATGACCCCGATGCGCTTCTTAGGC 30  
RESULT 2  
US-09-976-740-33  
Sequence 33, Application US/09976740  
Publication No. US2002019463A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/976,740  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-976-740-33

Alignment Scores:  
Pred. No.: 0.00149 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-976-740-22 (1-10) x US-09-976-740-33 (1-30)  
QY 1 GlusapaspapProaspGlypheLeuGly 10  
Db 1 GAGGATGATGACCCCGATGCGCTTCTTAGGC 30  
RESULT 3  
US-10-671-242-33  
Sequence 33, Application US/10671242  
Publication No. US2004004004A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/671,242  
CURRENT FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-671-242-33  
Alignment Scores:  
Pred. No.: 0.00149 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-976-740-22 (1-10) x US-10-671-242-33 (1-30)  
QY 1 GlusapaspapProaspGlypheLeuGly 10  
Db 1 GAGGATGATGACCCCGATGCGCTTCTTAGGC 30  
RESULT 4  
US-10-023-529-33  
Sequence 33, Application US/10023529  
Publication No. US20020129388A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS



FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-529-33

Alignment Scores:  
Pred. No.: 0.00149 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-976-740-22 (1-10) x US-10-023-529-33 (1-30)

QY 1 GluaspaspProaspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGCTTCTTAGGC 30

RESULT 5  
US-10-023-523-33  
Sequence 33, Application US/10023523  
Publication No. US20020152485A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,523  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-523-33

Alignment Scores:  
Pred. No.: 0.00149 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-09-976-740-22 (1-10) x US-10-023-523-33 (1-30)

QY 1 GluaspaspProaspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGCTTCTTAGGC 30

RESULT 6  
US-10-616-187-33  
Sequence 33, Application US/10616187  
Publication No. US20040003668A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/616,187  
CURRENT FILING DATE: 2003-07-09  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 30  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-616-187-33

Alignment Scores:  
Pred. No.: 0.00149 Length: 30  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-976-740-22 (1-10) x US-10-616-187-33 (1-30)

QY 1 GluaspaspProaspGlyPheLeuGly 10  
DB 1 GAGGATGATGACCCCGATGCTTCTTAGGC 30

RESULT 7  
US-09-962-055-16  
Sequence 16, Application US/09962055  
Patent No. US20020052033A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Robert S.  
APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston

```

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,055
FILING DATE: 24-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (Formerly 3983/5981B)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..651
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-962-055-16
Alignment Scores:
Pred. No.: 0.0557 Length: 1208
Score: 58.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-976-740-22 (1-10) x US-09-962-055-16 (1-1208)
QY 1 Gluaspaspapptcaspolyphenylc 10
Db 622 GAGGATGATGACCCGATGCTTCTTAGC 651
RESULT 8
US-09-976-740-16
Sequence 16: Application US/09976740
Publication No. US20020194633A1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING AND TREATING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53

```

```

SOFTWARE FastSeq for Windows Version 4.0
SRQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
US-09-976-740-16

Alignment Scores:
Pred. No.:
Score: 0.0557 Length: 1208
Percent Similarity: 100.00% Matches: 10
Best Local Similarity: 100.00% Conservative: 10
Query Match: 100.00% Mismatches: 0
DB: 9 Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-09-976-740-16 (1-1208)
Oy 1 GluAspAspAspProAspGlyPheLeuGly 10
|||
622 GAGGATGATGACCCCGATGCGCTTTTAGGC 651

RESULT 9
US-10-671-242-16
Sequence 16, Application US/10671242
Publication No. US20040040049A1
GENERAL INFORMATION:
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Ann M.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/671,242
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 1208
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(651)
US-10-671-242-16

Alignment Scores:
Pred. No.:
Score: 0.0557 Length: 1208
Percent Similarity: 100.00% Matches: 10
Best Local Similarity: 100.00% Conservative: 10
Query Match: 100.00% Mismatches: 0
DB: 12 Indels: 0
Gaps: 0

US-09-976-740-22 (1-10) x US-10-671-242-16 (1-1208)
Oy 1 GluAspAspAspProAspGlyPheLeuGly 10
|||
622 GAGGATGATGACCCCGATGCGCTTTTAGGC 651

```

```
RESULT 10
US-10-023-529-16
; Sequence 16, Application US/10023529
; Publication No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-023-529-16

Alignment Scores:
Pred. No.: 0.0557 Length: 1208
Score: 58.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-976-740-22 (1-10) x US-10-023-529-16 (1-1208)

QY 1 GluaspaspappproaspGlyPheLeuGly 10
Db 622 GAGGATGATGACCCGATGGCTTCTTAGGC 651

RESULT 11
US-10-023-523-16
; Sequence 16, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
```

```
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-023-523-16

Alignment Scores:
Pred. No.: 0.0557 Length: 1208
Score: 58.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0

US-09-976-740-22 (1-10) x US-10-616-187-16 (1-1208)

QY 1 GluaspaspappproaspGlyPheLeuGly 10
Db 622 GAGGATGATGACCCGATGGCTTCTTAGGC 651

RESULT 12
US-10-616-187-16
; Sequence 16, Application US/10616187
; Publication No. US20040013668A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/616,187
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1208
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(651)
US-10-616-187-16

Alignment Scores:
Pred. No.: 0.0557 Length: 1208
Score: 58.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
```

Oy 1 GluaspaspProaspGlyPheLeuGly 10  
DB 622 GAGATGATGACCCCGATGCTTCTTAGGC 651

RESULT 13

US-10-102-806-247  
; Sequence 247, Application US/10102806  
; Publication No. US20030054421A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA103P1C1  
; CURRENT APPLICATION NUMBER: US/10/102,806  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: 09/925,298  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05881  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 846  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 247  
; LENGTH: 1336  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (26)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (1336)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-102-806-247

Alignment Scores:

Pred. No.: 0 0615 Length: 1336  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-09-976-740-22 (1-10) x US-10-102-806-247 (1-1336)

Oy 1 GluaspaspProaspGlyPheLeuGly 10  
DB 694 GAGATGATGACCCCGATGCTTCTTAGGC 723

RESULT 14

US-09-945-527-6  
; Sequence 6, Application US/09945527  
; Publication No. US2003005588A1  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. US2003005588A1 Nucleic Acid Molecules Encoding  
; FILE REFERENCE: 35800/237985  
; CURRENT APPLICATION NUMBER: US/09/945,527  
; CURRENT FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1445  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-945-527-6

Alignment Scores:

Pred. No.: 0 0664 Length: 1445  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-09-976-740-22 (1-10) x US-09-945-527-6 (1-1445)

Oy 1 GluaspaspProaspGlyPheLeuGly 10  
DB 807 GAGATGATGACCCCGATGCTTCTTAGGC 836

RESULT 15

US-09-976-740-45  
; Sequence 45, Application US/09976740  
; Publication No. US20020194633A1  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Axtone, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/976,740  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 09/616,289  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 1614  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1614)  
US-09-976-740-45

Alignment Scores:

Pred. No.: 0 0741 Length: 1614  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-22 (1-10) x US-09-976-740-45 (1-1614)

Oy 1 GluaspaspProaspGlyPheLeuGly 10  
DB 1585 GAGATGATGACCCCGATGCTTCTTAGGC 1614

Search completed: March 13, 2004, 04:26:15  
Job time : 15.4676 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:55:37 ; Search time 151.2 Seconds  
(without alignments)  
1975.018 Million cell updates/sec

Title: US-09-976-740-22  
Perfect score: 58  
Sequence: 1 EDDPDGFLG 10

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n\_model -DEV=slp  
-O=/cgn2\_1/USPTO\_spool\_p/US09976740/runat\_10032004\_094548\_19551/app\_query.fasta\_1.1698  
-DB=BST -QFMT=fastap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=-1 -MATRIX=biolum62 -TRANS=human40.cdf -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976740@cgn2\_1\_10232@runat\_10032004\_094548\_19551 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=5 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:\*  
1: em\_eebha:\*  
2: em\_eeethum:\*  
3: em\_eeclin:\*  
4: em\_eeestm:\*  
5: em\_eeestov:\*  
6: em\_eeestpl:\*  
7: em\_eeestio:\*  
8: em\_eehrc:\*  
9: gb\_eeest1:\*  
10: gb\_eeest2:\*  
11: gb\_eeest3:\*  
12: gb\_eeest4:\*  
13: gb\_eeest5:\*  
14: gb\_eeest6:\*  
15: em\_eeestfun:\*  
16: em\_eeestom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	313	9 AA481593	AA481593 aa35606.r
2	58	100.0	361	14 D80440	D80440 HUM07AC06A
3	58	100.0	362	9 AA311602	AA311602 EST182332
4	58	100.0	406	12 BP432333	BP432333 BP432333
5	58	100.0	411	14 CB802479	CB802479 AMGNNUC:S
6	58	100.0	427	9 A1247702	A1247702 qn60h02.x
7	58	100.0	430	13 BQ317482	BQ317482 RCL-CT030
8	58	100.0	436	9 A1057236	A1057236 c21d06.x
9	58	100.0	454	9 A1198298	A1198298 q161d04.x
10	58	100.0	454	9 A1498877	A1498877 tm68h04.x
11	58	100.0	457	12 BM714074	BM714074 UI-E-EUO-
12	58	100.0	461	12 BM675258	BM675258 UI-E-EUO-
13	58	100.0	464	12 BM842690	BM842690 K-EST0120
14	58	100.0	464	12 BM842726	BM842726 K-EST0120
15	58	100.0	466	12 BM840318	BM840318 K-EST0117
16	58	100.0	469	14 R764998	R764998 y416h11.r
17	58	100.0	490	9 A1271358	A1271358 q103d11.x
18	58	100.0	491	10 BE696235	BE696235 RCL-CT030
19	58	100.0	537	12 B1838958	B1838958 603089250
20	58	100.0	538	14 CB717489	CB717489 AMGNNUC:N
21	58	100.0	557	14 CD673768	CD673768 fs04b02.y
22	58	100.0	558	12 BG827200	BG827200 602749308
23	58	100.0	611	10 BR334560	BR334560 RCL-CT030
24	58	100.0	632	12 B1114110	B1114110 602862629
25	58	100.0	663	10 AW611194	AW611194 RCL-CT030
26	58	100.0	692	13 BX118116	BX118116 BX118116
27	58	100.0	699	12 BG825632	BG825632 602749818
28	58	100.0	709	13 BQ190740	BQ190740 UI-R-DZ0-
29	58	100.0	719	13 BQ196255	BQ196255 UI-R-DZ0-
30	58	100.0	736	13 BQ200548	BQ200548 UI-R-DZ1-
31	58	100.0	748	10 BG031920	BG031920 602300612
32	58	100.0	756	12 BM013469	BM013469 603638922
33	58	100.0	764	13 BQ445960	BQ445960 UI-R-EU1-
34	58	100.0	780	14 CB325238	CB325238 UI-R-DZ0-
35	58	100.0	785	12 B1226646	B1226646 602951660
36	58	100.0	795	14 CB324552	CB324552 UI-R-DZ0-
37	58	100.0	799	13 BU620639	BU620639 UI-R-FL1-
38	58	100.0	812	12 BG762763	BG762763 602734678
39	58	100.0	829	10 BE270987	BE270987 600943804
40	58	100.0	862	13 BQ673964	BQ673964 AGENCOURT
41	58	100.0	1109	10 BE270805	BE270805 600943804
42	54	93.1	461	12 B1305052	B1305052 AR068D101
43	54	93.1	534	10 AM669983	AM669983 113863 MA
44	54	93.1	592	12 B1343168	B1343168 371223 MA
45	53	91.4	255	13 BQ084241	BQ084241 K-EST0148

## ALIGNMENTS

RESULT 1  
AA481593/c 313 bp mRNA EST 14-AUG-1997  
aa35606.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:815266 5',  
LOCUS  
DEFINITION  
ACCESSION AA481593  
VERSION AA481593.1 GI:2211145  
KEYWORDS  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 313)



Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse.

## FEATURES

## source

1. 362  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="ATCC (Inhost):158827"  
 /db\_xref="taxon:9606"  
 /cell\_type="T-Lymphocyte"  
 /clone\_id="Jurkat T-cells VI"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI"

## ORIGIN

## Alignment Scores:

Pred. No.: 2.34 Length: 362  
 Score: 58.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-976-740-22 (1-10) x AA311602 (1-362)

Qy 1 GUASPAPSPProAspGlyPheLeuGly 10  
 |||||  
 Db 305 GAGGATGATGACCCGATGGCTTCTTAGGC 334

## RESULT 4

## BP432333

## LOCUS

BP432333 leukemia cell normalized cDNA library Homo sapiens cDNA

clone LEU4076\_8.D5, mRNA sequence.

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

## JOURNAL

## MEDLINE

## COMMENT

## JOURNAL

## MEDLINE

## COMMENT

## JOURNAL

## MEDLINE

## COMMENT

## JOURNAL

## MEDLINE

## COMMENT

## JOURNAL

## MEDLINE

## COMMENT

## JOURNAL

## MEDLINE

## COMMENT

Pred. No.: 2.67 Length: 406  
 Score: 58.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 12 Gaps: 0

US-09-976-740-22 (1-10) x BP432333 (1-406)

Qy 1 GUASPAPSPProAspGlyPheLeuGly 10  
 |||||  
 Db 246 GAGGATGATGACCCGATGGCTTCTTAGGC 275

RESULT 5  
 CB802479  
 LOCUS  
 DEFINITION  
 AMGNNUC:SRPB2-00295-B1-A srpb2 (10220) Rattus norvegicus cDNA clone  
 srpb2-00295-b1 5', mRNA sequence.

ACCESSION  
 CB802479.1 GI:29916753

VERSION  
 CB802479.1 GI:29916753

KEYWORDS  
 EST.

SOURCE  
 Rattus norvegicus (Norway rat)

ORGANISM  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Scleroglossi; Muridae; Murinae;  
 Rattus.

REFERENCE  
 1 (bases 1 to 411)  
 Amgen EST Program.  
 TITLE  
 JOURNAL  
 COMMENT  
 Amgen, Inc  
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00295 row: b column: 1.

FEATURES  
 source  
 1. 411  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="srpb2-00295-b1"  
 /tissue\_type="prostate tissue"  
 /clone\_id="srpb2 (10220)"  
 /note="Vector: pSPORF1; Site\_1: SalI; Site\_2: NotI; rat  
 prostate normalized double selected poly(A+) mRNA size  
 fraction > 1 kb"

ORIGIN

Alignment Scores:

Pred. No.: 2.7 Length: 411  
 Score: 58.00 Matches: 10  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

US-09-976-740-22 (1-10) x CB802479 (1-411)

Qy 1 GUASPAPSPProAspGlyPheLeuGly 10  
 |||||  
 Db 184 GAGGACGATGATCCGATGGCTTCTTAGGC 213

RESULT 6  
 A1247702/c  
 LOCUS  
 DEFINITION  
 qh6h02.x1 Soares fetal liver spleen tNLS S1 Homo sapiens cDNA  
 clone IMAGE:1849107 3', similar to TR:P78365 P78365 POLYHOMEOTIC 2  
 HOWOLOG: ;, mRNA sequence.

ACCESSION  
 A1247702

VERSION  
 A1247702.1 GI:3843099

KEYWORDS  
 EST.

SOURCE  
 Homo sapiens (human)

ORGANISM  
 Homo sapiens

## Alignment Scores:

**REFERENCE**  
1 (bases 1 to 427)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**AUTHORS**  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
**JOURNAL**  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 587 Std Error: 0.00  
Seq primer: -40UP from G4bc  
High quality sequence stop: 349.  
**FEATURES**  
Location/Qualifiers  
1..427  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1849107"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares\_fetal\_liver\_spleen\_INFLS\_S1"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
This is a subtracted version of the original Soares fetal  
liver spleen INFLS library. 1st strand cDNA was primed  
with a Pac I - oligo(dT) primer [5',  
ACTGGAGAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Benito Soares and M. Fatima Bonaldo."

**ORIGIN**  
Alignment Scores:  
Pred. No.: 2.82 Length: 427  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x A1247702 (1-427)

**Qy**  
1 GUAASPAPSPProASPgiYPheLeugly 10  
|||||  
Db 289 GAGGATGATGACCCCGATGCGCTTTAGGC 260

**RESULT 7**  
BQ317482 430 bp mRNA linear EST 17-MAY-2002  
LOCUS R01-CT0302-040400-017-d09 CT0302 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BQ317482  
ACCESSION BQ317482  
VERSION BQ317482.1 GI:20923251  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 430)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663

**TITLE**  
JOURNAL  
MEDLINE

**PUBMED**  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC1&t2=RC1-CT0302-040400-017-d09&t3=2000-04-04&t4=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 23.  
**FEATURES**  
Location/Qualifiers  
1..430  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="CT0302"  
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORS875 PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

**ORIGIN**  
Alignment Scores:  
Pred. No.: 2.84 Length: 430  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-22 (1-10) x BQ317482 (1-430)

**Qy**  
1 GUAASPAPSPProASPgiYPheLeugly 10  
|||||  
Db 144 GAGGATGATGACCCCGATGCGCTTTAGGC 173

**RESULT 8**  
A1057236 436 bp mRNA linear EST 29-SEP-1998  
LOCUS oz11d06.x1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA  
DEFINITION clone IMAGE:1675019 3' similar to TR:P78365 P78365 POLYHOMERIC 2  
HOMOLOG. ; mRNA sequence.  
ACCESSION A1057236  
VERSION A1057236.1 GI:3331102  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 436)  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Insert Length: 593 Std Error: 0.00  
Seq primer: -40m13 fwd. BT from Amersham  
High quality sequence stop: 351.  
**FEATURES**  
Location/Qualifiers  
1..436  
/organism="Homo sapiens"

**TITLE**  
JOURNAL  
MEDLINE



/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1675019"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="MDH10B (ampicillin resistant)"  
/clone\_lib="Soares\_fetal\_liver\_infls\_S1"  
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)  
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
This is a subtracted version of the original Soares fetal  
liver spleen INFLS library. 1st strand cDNA was primed  
with a Pac I - oligo(dT) primer [5',  
AAGTGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.89 Length: 436  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-22 (1-10) x A1057236 (1-436)

Cy 1 GluaspaspappproaspGlyPheLeugly 10  
Db 289 GAGATGATGACCCGATGCTTCTTAGGC 260

## RESULT 9

A1198288/c 454 bp mRNA linear EST 02-DEC-1998  
LOCUS A1198288  
DEFINITION g16104.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:1860967 3'  
similar to TR:P78365 P78365 POLYHOMEOTIC 2 HOMOLOG. ;, mRNA  
sequence.

ACCESSION A1198288  
VERSION A1198288.1 GI:3750894  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 454)  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index

JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lemmon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdip/image/image.html  
Insert length: 685 Std Error: 0.00  
Seq primer: -40UP from Gldco  
High quality sequence stop: 374.

## FEATURES

Source  
1..454  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1860967"

/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="MDH10B"  
/clone\_lib="NCI CGAP Brn25"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTCACATCGAAGTGGAGCGCCGATGCTTTTCTTTTCTTTT  
T 3')]; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M.Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.02 Length: 454  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-22 (1-10) x A1198288 (1-454)

Cy 1 GluaspaspappproaspGlyPheLeugly 10  
Db 301 GAGATGATGACCCGATGCTTCTTAGGC 272

RESULT 10  
A1498877 454 bp mRNA linear EST 14-APR-1999  
LOCUS A1498877/c  
DEFINITION tm68H04.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2163319 3'  
similar to TR:P78365 P78365 POLYHOMEOTIC 2 HOMOLOG. ;, mRNA  
sequence.

ACCESSION A1498877  
VERSION A1498877.1 GI:4390859  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 454)  
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index

JOURNAL Unpublished (1998)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lemmon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bdip/image/image.html  
Insert length: 698 Std Error: 0.00  
Seq primer: -40UP from Gldco  
High quality sequence stop: 372.

## FEATURES

Source  
1..454  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2163319"  
/tissue\_type="anaplastic oligodendroglioma"  
/lab\_host="MDH10B"  
/clone\_lib="NCI CGAP Brn25"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'

## ORIGIN

TTTACCAATCTGAGTGGAGCGCCGATAGCTTTTTTTTTTTTTTTTTTTTTT  
 T 3']: double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT73 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M.Faciola Bonaldo.

## Alignment Scores:

Pred. No.:	Length:	454
Score:	58.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	9	Gaps:

US-09-976-740-22 (1-10) x A1498877 (1-454)

Cy 1 GluAspAspAspProAspGlyPheLeuGly 10

Db 301 GAGAGTATGATGACCCGATGCTTTTAGGC 272

## RESULT 11

BM714074 457 bp mRNA linear EST 28-FEB-2002  
 LOCUS UI-E-EJ0-ahr-h-07-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone

ACCESSION EM714074.1 GI:19027332

VERSION EM714074.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 457)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: Bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Reverse.

Location/Qualifiers

1..457

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-EJ0-ahr-h-07-0-UI"

/tissue\_type="fetal eyes, lens, eye anterior segment,"

optic nerve, retina, Retina Foveal and Macular, RPE and

Choroid"

/dev\_stage="fetal and adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-EJ0"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a

modified polylinker; Site\_1: EcoR I; Site\_2: Not I;

UI-E-EJ0 is a subtracted cDNA library constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested

with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dr)18 tail. The  
 sequence tags for this library are: fetal eyes,  
 AGAATCAAGA, lens, CCATTAGCA, eye anterior segment,  
 AATCCGCAT, optic nerve, CCATTAGTG, retina, CCGCG, Retina  
 Foveal and Macular, GTCC, RPE and Choroid, ACCTA. This  
 library was created for the program, Gene Discovery in the  
 Visual System, supported by National Eye Institute (NEI)."

## ORIGIN

Pred. No.:	Length:	457
Score:	58.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	12	Gaps:

US-09-976-740-22 (1-10) x EM714074 (1-457)

Cy 1 GluAspAspAspProAspGlyPheLeuGly 10

Db 149 GAGATATGATGACCCGATGCTTTTAGGC 178

## RESULT 12

BM675258 461 bp mRNA linear EST 27-FEB-2002  
 LOCUS UI-E-EJ0-ahr-h-07-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone

ACCESSION BM675258.1 GI:18985156

VERSION BM675258.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 461)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: Bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

Seq primer: M13 Forward

Location/Qualifiers

1..461

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-E-EJ0-ahr-h-07-0-UI"

/tissue\_type="fetal eyes, lens, eye anterior segment,"

optic nerve, retina, Retina Foveal and Macular, RPE and

Choroid"

/dev\_stage="fetal and adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-EJ0"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-E-Eco is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATTCAGCA; lens, CGATTAGCG; eye anterior segment, AATGCCGAT; optic nerve, CCATTAGCG; retina, CCGCG; Retina Foveal and Macular, GTCG; RPE and Choroid, ACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI). TAG TISSUE-human retina  
TAG LIB=UI-E-Eco  
TAG\_SEQ=CCGCG"

## ORIGIN

Alignment Scores:  
Pred. No.: 3.08 Length: 461  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-976-740-22 (1-10) x BM675258 (1-461)

Oy 1 GUAASPAPSPROASPGLYPHELUGLY 10  
Db 304 GAGGATGATGACCCCGATGCTTCTTAGGC 275

## RESULT 13

BM842690

LOCUS K-EST0120140 S12SN216 Homo sapiens cDNA clone S12SN216-66-F06 5',  
DEFINITION mRNA sequence.  
ACCESSION BM842690 464 bp mRNA linear EST 06-MAR-2002  
VERSION BM842690.1 GI:19199099

KEYWORDS EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 66 row: F column: 06  
High quality sequence stop: 464.  
Location/Qualifiers  
1. 464

## FEATURES

source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S12SN216-66-F06"  
/sex="F"  
/tissue\_type="Lymph node"  
/cell\_type="Epithelial"  
/cell\_line="SNV-216"  
/clone\_lib="S12SN216"

/lab\_host="Top10F"  
/clone\_lib="S12SN216"  
/note="Organ: Stomach; Vector: pcnS; Site 1: EcoRI; Site 2: NotI. The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tabacco acid pyrophosphatase (TAP). The deacapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoR which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.1 Length: 464  
Score: 58.00 Matches: 10  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-976-740-22 (1-10) x BM842690 (1-464)

Oy 1 GUAASPAPSPROASPGLYPHELUGLY 10  
Db 249 GAGGATGATGACCCCGATGCTTCTTAGGC 278

## RESULT 14

BM842726

LOCUS K-EST0120184 S12SN216 Homo sapiens cDNA clone S12SN216-66-B02 5',  
DEFINITION mRNA sequence.  
ACCESSION BM842726 464 bp mRNA linear EST 06-MAR-2002  
VERSION BM842726.1 GI:19199135

KEYWORDS EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 66 row: B column: 02  
High quality sequence stop: 464.  
Location/Qualifiers  
1. 464

## FEATURES

source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S12SN216-66-B02"  
/sex="F"  
/tissue\_type="Lymph node"  
/cell\_type="Epithelial"  
/cell\_line="SNV-216"  
/lab\_host="Top10F"  
/clone\_lib="S12SN216"

/note="Organ: Stomach; Vector: pCNS; Site: 1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.1	464	58.00	10	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:		100.00%					
DB:	12						

US-09-976-740-22 (1-10) x BM842726 (1-464)

Qy 1 GluaspaspaspProaspGlyPheLeuGly 10

Db 249 GAGGATGATGACCCCGATGGCTTCTTAGGC 278

## RESULT 15

BM840318

LOCUS 466 bp mRNA linear EST 06-MAR-2002

DEFINITION K-EST0117357 S12SNU216 Homo sapiens cDNA clone S12SNU216-41-E05 5',

mRNA sequence.

ACCESSION BM840318

VERSION BM840318.1 GI:19196727

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens (human); Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 466)

REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

AUTHORS Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

ZIC Frontier Korean EST Project 2001

Unpublished (2002)

JOURNAL Contact: Kim YS

COMMENT Genome Research Center

Korea Research Institute of Bioscience &amp; Biotechnology

52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 41 row: E column: 05

High quality sequence stop: 466.

Location/Qualifiers

FEATURES:

SOURCE

1..466

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S12SNU216-41-E05"

/sex="F"

/tissue\_type="Lymph node"

/cell\_type="Epithelial"

/cell\_line="STU-216"

/lab\_host="Top10F"

/clone\_id="S12SNU216"

/note="Organ: Stomach; Vector: pCNS; Site: 1: EcoRI;

Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.11	466	58.00	10	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:		100.00%					
DB:	12						

US-09-976-740-22 (1-10) x BM840318 (1-466)

Qy 1 GluaspaspaspProaspGlyPheLeuGly 10

Db 249 GAGGATGATGACCCCGATGGCTTCTTAGGC 278

Search completed: March 13, 2004, 04:01:47  
Job time : 157.2 secs











ID AAH26489 standard; cDNA; 1362 BP.  
AC AAH26489;  
XX  
XX  
DT 12-NOV-2001 (first entry)  
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
XX  
XX Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit;  
KM atherosclerosis; arteriosclerosis; gene therapy; diagnosis; vaccine;  
KM ss.  
XX  
XX Oryctolagus cuniculus.  
OS  
FH Key Location/Qualifiers  
FT CDS l..955  
FT /tag= a  
FT /partial  
FN W0200164874-A2.  
PN  
PD 07-SEP-2001.  
PF 28-FEB-2001; 2001WO-US006356.  
PR 02-MAR-2000; 2000US-00517849.  
PR 14-JUL-2000; 2000US-00616289.  
XX  
PA (BOST-) BOSTON HEART FOUND INC.  
PI Lees AM, Lees RS, Law SW, Arjona AA;  
DR WPI; 2001-565505/63.  
DR P-PADB; AAB82799.  
XX  
XX  
PT New isolated low density lipoprotein binding polypeptide for treating,  
PS diagnosing and/or identifying therapeutic agents for atherosclerosis.  
XX  
XX Example 2; Fig 12; 143bp; English.

The present sequence is that of cDNA encoding a portion (see AAB82799) of novel rabbit low density lipoprotein binding protein 2 (LBP-2). The cDNA was isolated following screening of a rabbit cDNA library for clones encoding LBPs that bound to both native low density lipoprotein (LDL) and methyl LDL. A full-length sequence for LBP-2 is given in AAH26500. The invention provides claimed polynucleotides encoding novel polypeptides which are capable of binding to native and methylated LDL, the isolated polypeptides, termed LBPs, and biologically active fragments and analogues of them, as well as expression vectors, cells and methods of producing the LBPs. Also claimed are methods for evaluating if an animal is at risk for atherosclerosis, methods for determining if an animal is in treating atherosclerosis, and methods for treating a cell having an abnormality in structure or metabolism of LBP. Pharmaceutical compositions comprising an LBP polypeptide or nucleic acid, and vaccine compositions, are also claimed

Sequence 1362 BP; 259 A; 421 C; 419 G; 263 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 7.15e-53 Length: 1362  
Score: 1047.50 Matches: 195  
Percent Similarity: 95.45% Conservative: 15  
Best Local Similarity: 88.64% Mismatches: 7  
Query Match: 89.53% Indels: 3  
DB: 5 Gaps: 2

US-09-976-740-7 (1-217) x AAH26489 (1-1362)

```

QY      1  GIUGIUAAGYAlleuglulurysgluglugluAAspAspGluAspGluAspGlu 20
Db      37  GAGAGAGCAAGTGGTTGAAGAGCGAGCGAGCGAGCGAGCGAGAAAGAGCAGAGCAGAC   96
        |||.....|.....|.....|.....|.....|.....|.....|.....|.....|
        21 AspAsp-----ValserGIUGIYserGIUValProglUserAspArgProalGIyAla 38

```

Dd		97	GACGAGCACTCGTCCGAGGGCTCGAGGTGCCGAGAGCATCGTCCCGGGTGCG	156
Oy		39	GLNHSHSGINLEUEN---GLYLHARGGLYPROGINSERIALVSGILNARYVALYS	57
Dd		157	CAGATTCACCAAGCTGAATGAGCGCAGCGCGGCCTCCGACCGCCMAAGACGGSCCAG	216
Oy		58	GIUTPThrProCysGlyProHisGlnGlyAsnGlyIUGLYARGLYProlAproGly	77
Dd		217	GAGGTGCGGTGTGTGTGCCCCCACCTCGCCACGAGAGAAGGCGGGGCGCCGCGCGC	278
Oy		78	SerGlyThrArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSer	97
Dd		277	AGTGGCACCCCGCAGGTTGTTCTCCATGCGGCGCTTAGTAAGAGGGGGGATCAGCTCT	336
Oy		98	ValAlaThrGlyProAspSerProSerProValP.Proleup.ProProGlyLysProAlaLeu	111
Dd		337	TGCACCACGGGACTTACTCCCGTCCCGGTGCTTGCCCGCGGAAAGCCAGCCCTC	396
Oy		118	ProGlyAlaAspGlyThrProPheGlyCysProProGlyIARGLYsgLULysProSerAsp	137
Dd		397	CCAGGAGCGGATGGAGACCCCTTTGGCTGCTCGCGCGGCGCCAAAGAGAACCCGAGAC	456
Oy		138	ProValGluThrPhrThalMetAspValValGluTrpMetThrGluAlaGlyPheProGlu	151
Dd		457	CCGTGGAGGAGCACTCATGAGACGTCTGGAGTACTTCACCGAGGCGGGCTTCTCTGAG	518
Oy		158	GlnAlaThrAlaPheGlnGluGlnIleAspGlyLysSerLeuLeuMetGlnArg	177
Dd		517	CAGGCCACGGCTTCCAGGAGGACGAGANTCAGCGCAAGTCCCTGCTGCTCATGCAAGC	576
Oy		178	ThrAspValIeuThrGlyLeuSerIleArgLeuGlyP.ProlAleuLysIleTYrGluHis	197
Dd		577	ACGAGTGTCTCTCACCGGCTGTCTCATCCGCTCGGGGCGCAGCGTTGAAMATTATGAGCAC	636
Oy		198	HISlleLysValLeuGlnGlnIleHisPheGluAspAspAspProAspGlyPheLeuGly	217
Dd		637	CATTCAAGGTGCTGCAGCAGGAGTCACTTCGAGACGATGACCCGGAAGGCTTCTCTGGA	696
<b>RESULT 6</b>				
ID	AAH26490			
	AAH26490 standard; cDNA; 1422 BP.			
XX	AAH26490;			
AC				
XX				
DT	12-NOV-2001 (first entry)			
XX				
DE	Rabbit low density lipoprotein binding protein 3 (LBP-3) cDNA.			
XX				
KM	Low density lipoprotein binding protein 3; LBP-3; LDL; rabbit; atherosclerosis; antiatherosclerotic; gene therapy; diagnosis; vaccine; ss.			
OS	Oryctolagus cuniculus.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..985		
FT		/+tag= a		
FT		/partial		
PN	W0200164874-A2.			
PD				
XX	07-SEP-2001.			
PF	28-FEB-2001; 2001MO-US006356.			
XX				
PR	02-MAR-2000; 2000US-00517845.			
XX	14-JUL-2000; 2000US-00616285.			
PA	(BOST-) BOSTON HEART FOUND INC.			
PI	Lees AM, Lees RS, Law SM, Arizona AA;			
XX				



Best Local Similarity: 88.64% Mismatches: 7  
 Query Match: 89.53% Indels: 3  
 DB: 5 Gaps: 2

US-09-976-740-7 (1-217) x AAH26488 (1-1617)

```

QY 1 GIUGLUARGVALLLEUGLULYSGLUGLUGLUUASPAPSPGLUASPGLUASPGLU 20
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 292 GAGAGAGGAGTGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
QY 21 ASPASP-----VALSERGLUGLYSERGLUVALPROGLUSERAPSPROALAGLYALA 38
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 GACGACGACGCTGCTGCTCGAGAGGCTCGAGAGTCCCGAGAGCATCTCTCCCGGGTGGC 411
QY 39 GLHISHSISGLINLEUASN---GLYGLUARGLYPROGLINERLALYSGLUARGLY 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 412 CAGCATACCACTGATGGCGCGGACCGCGCCCGGACACCCCGCAGAGAGCGCGCAG 471
QY 58 GLUTPThrProCysGlyProHisGlnGlyGlnASPGLUARGLYProAlaProGly 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 472 GAGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531
QY 78 SERGLYThrArgGlnValPheSerMetAlaAlaMetAsnLysGlnGlyGlyThrAlaSer 97
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 532 AGTGGCACCCGCGCGAGTGTCTCCATGCGCGCTTGAAGAAGAGGGGGATCAGCCTCT 591
QY 98 VALALAThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 592 TCGACACCGGGGCTGACTCCCGGTCCCGGTGCTTGGCCCCCGGGAAGCCAGCCCTC 651
QY 118 PROGLYALAASPGLYThrProPheGlyCysProProGlyArgLysGlnLysProSerASP 137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 652 CCAAGACCCGATGGAGACCCCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 711
QY 138 PROVALGluTrpThrValMetAspValValGluTrpPheThrGlnAlaGlyPheProGly 157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 712 CCCGTGAGTGCAGACGATCAGACGCTGTGAGAGTCTTCCAGAGCGGGCTTCCCTGAG 771
QY 158 GlnAlaThrAlaPheGlnGlnGlnGlnLysASPGLYLysSerLeuLeuLeuMetGlnArg 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 772 CAAAGCCACGGCTTCCAGAGACAGAGATCAGACGGCAGATCCCTGCTGCTCATGCAAGC 831
QY 178 ThrAspValLeuThrGlyLeuSerLeuArgLeuGlyProAlaLeuLysLeuArgLys 197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 832 ACCGATGCTCTCAGCGGCTGCTCCATCGCTGCGGCGACGCTGAAATCTATGAGAC 891
QY 198 HISLIEHSISGLINLEUASN---GLYGLUARGLYProGlnSerLALYSGLUARGLY 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 892 CATATCAAGTGTGCGACGAGGCTCACTCGAGGACATACCCCGAAGCTTCCCTGAG 951

```

RESULT 8

AAH26500 standard; cDNA; 2561 BP.

AAH26500;

12-NOV-2001 (first entry)

Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.

Low density lipoprotein binding protein 2; LBP-2; LDL; rabbit; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

ss.

Oryctolagus cuniculus.

Key Location/Qualifiers

246..1928

MO200164874-A2.

```

XX 26-FEB-2001; 2001MO-US006356.
XX
XX 02-MAR-2000; 2000US-00517849.
XX 14-JUL-2000; 2000US-00616289.
XX
XX (BOST-) BOSTON HEART FOUND INC.
XX
XX Lees AM, Lees RS, Law SW, Arjona AA,
XX WPI, 2001-565505/63.
XX P-PSDB; AAH82807.
XX
XX New isolated low density lipoprotein binding polypeptide for treating,
XX diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX Claim 4; Fig 2A; 143pp; English.
XX
XX The present sequence is that of cDNA encoding novel rabbit low density
XX lipoprotein binding protein 1 (LBP-2, see AAH82807). The cDNA was
XX isolated following screening of a rabbit cDNA library for clones encoding
XX LBPs that bound to both native low density lipoprotein (LDL) and methyl
XX LDL. The invention provides claimed polynucleotides encoding novel
XX polypeptides which are capable of binding to native and methylated LDL,
XX the isolated polypeptides, termed LBPs, and biologically active fragments
XX and analogues of them, as well as expression vectors, cells and methods
XX of producing the LBPs. Also claimed are methods of determining if an
XX animal is at risk for atherosclerosis, methods for evaluating an agent
XX for use in treating atherosclerosis, and methods for treating a cell
XX having an abnormality in structure or metabolism of LBP. Pharmaceutical
XX compositions comprising an LBP polypeptide or nucleic acid, and vaccine
XX compositions, are also claimed
XX
XX Sequence 2561 BP; 372 A; 937 G; 879 G; 373 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1 328-52 Length: 2561
XX Score: 1047.50 Matches: 195
XX Percent Similarity: 95.45% Conservative: 15
XX Best Local Similarity: 88.64% Mismatches: 7
XX Query Match: 89.53% Indels: 3
XX DB: 5 Gaps: 2

```

US-09-976-740-7 (1-217) x AAH26500 (1-2561)

```

QY 1 GIUGLUARGVALLLEUGLULYSGLUGLUGLUUASPAPSPGLUASPGLUASPGLU 20
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Db 1236 GAGAGAGGAGTGTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1295
QY 21 ASPASP-----VALSERGLUGLYSERGLUVALPROGLUSERAPSPROALAGLYALA 38
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1296 GACGACGACGCTGCTGCTCGAGAGGCTCGAGAGTCCCGAGAGCATCTCTCCCGGGTGGC 1355
QY 39 GLHISHSISGLINLEUASN---GLYGLUARGLYProGlnSerLALYSGLUARGLY 57
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1356 CAGCATACCACTGATGGCGGCGGACCGCGCCGACAGCCGCAAGAGAGCGGGCCAAAG 1415
QY 58 GLUTPThrProCysGlyProHisGlnGlyGlnASPGLUARGLYProAlaProGly 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1416 GAGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1475
QY 78 SERGLYThrArgGlnValPheSerMetAlaAlaMetAsnLysGlnGlyGlyThrAlaSer 97
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QY 98 VALALAThrGlyProAspSerProSerProValProLeuProProGlyLysProAlaLeu 117
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QY 118 PROGLYALAASPGLYThrProPheGlyCysProProGlyArgLysGlnLysProSerASP 137
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Dl		892 CATTCAGAGTGTCTGCACAGGGATCACTTGAGCAGCATGCCCGAAAGCTTCC763GA 951
<hr/>		
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XX	AAB26495 standard; DNA; 12425 BP.	
XX AC	AAB26495;	
DT	12-NOV-2001 (first entry)	
DE XX	Human low density lipoprotein binding protein 2 (LBP-2) gene.	
XX KM	Low density lipoprotein binding protein 2; LBP-2; LDL; human; atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine; ds.	
XX OS	Homo sapiens.	
FH FH	Key Location/Qualifiers	
CDS CDS	2832..5153	
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FT FT	/**tag= f	
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FT FT	/**tag= g	
FT exon	4788..4899	
FT intron	/**tag= h	
FT FT	4900..4994	
FT exon	/**tag= i	
FT FT	4995..5153	
FT FT	/**tag= j	
PX PX	W0200164874-A2.	
PD PD	07-SEP-2001.	
PF PF	28-FEB-2001; 2001MO-USO06356.	
PR PR	02-MAR-2000; 2000US-00517843.	
RR RR	14-JUL-2000; 2000US-00616289.	
PA PA	(BOST-) BOSTON HEART FOUND INC.	
PI PI	Lees AM, Lees RS, Law SW, Arjona AA;	
DR DR	WPJ; 2001-565505/63.	
PX PX	P-PSDS; AAB82806.	
PT PT	New isolated low density lipoprotein binding polypeptide for treating,	
PS PS	diagnosing and/or identifying therapeutic agents for arteriosclerosis.	
Example 4; Fig 23; 143bp; English.		
The present sequence is that of genomic DNA encoding novel human low density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was isolated from a human genomic library by screening with LBP-2 cDNA (see AAB26494). The open reading frame spans 5 exons. Human LBP-2 nucleic acid are among claimed polynucleotides of the invention that encode novel polypeptides, termed LBPs, capable of binding to native and methyiated LDL. Also claimed are isolated LBP polypeptides,, and		

[illegible]









XX DNA encoding novel human diagnostic protein #11304.  
DE  
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX WO200175067-A2.  
XX  
XX 11-OCT-2001.  
XX  
XX 30-MAR-2001; 2001WO-US008631.  
XX  
XX 31-MAR-2000; 2000US-00540217.  
XX 23-AUG-2000; 2000US-00649167.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Dmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-633362/73.  
XX P-PSDB; ABG11313.  
XX  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
XX  
XX Claim 1; SEQ ID NO 11304; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX  
XX Sequence 483 BP; 127 A; 112 C; 87 G; 157 T; 0 U; 0 Other;  
SQ  
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XX  
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Score: 285.00 Matches: 60  
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Best Local Similarity: 46.88% Mismatches: 26  
Query Match: 24.36% Indels: 28  
DB: 5 Gaps: 2  
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QY 103 AspSerProSerProValProLeuProGlyLysProAlaLeuProGlyAlaAspGly 122  
DB 336 GAAAT----- 331

QY 123 ThrProPheGlyCysProProGlyLysGluLysProSerAspProValAluTrpThr 142  
DB 330 -----GGGAGA-----CCACTGATCTCGACAGCTGGGCC 301  
QY 143 ValMetAspValValGluTyrPheThrGluAlaGlyPheProGluAlaThrAlaPhe 162  
DB 300 GTGATGATGTGCTCATTATTTCGACACCGTGGGATTGAGAGCAAGCTAGTGCTTT 241  
QY 163 GlnGlnGlnGluIleAspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThr 182  
DB 240 CAGGAACAGAAATTCATGAGAAATCCCTGCTATTGATCACAAGAAATGATGTGGACA 181  
QY 183 GlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLysValLeu 202  
DB 180 GGACTTCAGTTAAATTTGGGCTGCTCGAAATCTACGAATATCATGTAATAAACCCTTG 121  
QY 203 GlnGlnGlyHisPheGluAspAsp 210  
DB 120 CAGACAAAGCATTTAAGAACAAAC 97

Search completed: March 12, 2004, 21:08:21  
Job time : 357.96 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:49:56 ; Search time 3295.9 Seconds

(without alignments)  
2853.675 Million cell updates/sec

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Perfect score: 1170  
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Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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11: gb Sts:\*  
12: gb Sy:\*  
13: gb Un:\*  
14: gb Vi:\*  
15: em Ba:\*  
16: em Fun:\*  
17: em Hum:\*  
18: em In:\*  
19: em Mu:\*  
20: em Om:\*  
21: em Or:\*  
22: em Ov:\*  
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25: em Pl:\*  
26: em Ro:\*  
27: em Sts:\*  
28: em Un:\*

29: em vl:\*  
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32: em hrg other:\*  
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36: em hrg mam:\*  
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41: em htgo other:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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13	1047.5	89.5	1362	6 AR409318	AR409318 Sequence
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16	1047.5	89.5	1422	6 AR199532	AR199532 Sequence
17	1047.5	89.5	1422	6 AR374684	AR374684 Sequence
18	1047.5	89.5	1422	6 AR409319	AR409319 Sequence
19	1047.5	89.5	1422	6 AX239570	AX239570 Sequence
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22	1047.5	89.5	1617	6 AR374682	AR374682 Sequence
23	1047.5	89.5	1617	6 AR409317	AR409317 Sequence
24	1047.5	89.5	1617	6 AX239568	AX239568 Sequence
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27	1047.5	89.5	2561	6 AR409339	AR409339 Sequence
28	1047.5	89.5	2561	6 AX239605	AX239605 Sequence
29	1036.5	88.6	12425	6 AR409341	AR409341 Sequence
30	1036.5	88.6	12425	6 AX239607	AX239607 Sequence
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RESULT 1

ALIGNMENTS

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LOCUS BC007384 982 bp mRNA linear PRI 16-SEP-2003  
DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone  
IMAGE:3677194), partial cds.  
ACCESSION BC007384  
VERSION BC007384.2  
KEYWORDS GI:33988219  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
1 (bases 1 to 982)  
Krausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Martusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, A.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abrams, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,  
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huiyk, S.W.,  
Vallion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
2 (bases 1 to 982)  
22388257  
12477932  
JOURNAL Strausberg, R.  
MEDLINE Direct Submission  
PUBMED Submitted (01-MAY-2001) National Institutes of Health, Mammalian  
REFERENCE Gene Collection (MGC), Cancer Genomics Office, National Cancer  
AUTHORS Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
TITLE USA  
JOURNAL NIA-MGC Project URL: <http://mgc.ncl.nih.gov>  
REMARK On Aug 20, 2003 this sequence version replaced gi:13938477.  
COMMENT Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
contact: [amad@systemsbiology.org](mailto:amad@systemsbiology.org)  
Anup Madan, Jessica Fahy, Erin Helton, Mark Kettelman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
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Query Match: 100.00% Indels: 0  
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Db 58 GAAGAGCAGACTCTTGAAGAAAGAGAGAGAGATATATAGATGAGATGAGAA 117  
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Db 118 GATGATGTCAGAGGGCTCTGAAGTCCGAGAGTGACCGTCTGAGGTCACAGCAC 177  
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Db 418 GACGGGACCCCTTGGCTGTCTCCCGGGCGCAAGAGCATGTGATCCCGTGCAG 477  
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Db 598 CTCACGCGCGCTGTCATCCGCTCGGCGCAGCCCTGAATTCACGAGCCACATCAAG 657  
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VERSION	AX239573.1		
KEYWORDS	GI:15797257		
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	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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AUTHORS	1		
TITLE	Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.		
JOURNAL	Low density liprotein binding proteins and their use in diagnosing and treating atherosclerosis		
	Patent: WO 0164874-A 16 07-SEP-2001;		
	Boston Heart Foundation, Inc. (US)		
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ORIGIN			
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Qy	21	AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis	40
Db	61	GATGATGTGTCAAGAGGCTCTGAAGTCCCGAGAGTACCCGTCTCGAGGTGCCAGCAC	120
Qy	41	HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaLysGluArgValLysGluTyrThr	60
Db	121	CACCAAGCTTAACGGCGAGCGGAGACCTCAAGATGCCAAGAGAGAGGGTCAAGAGATGAC	180
Qy	61	ProCysGlyProHisGlnGlyGlnAsnGluGlyArgGlyProAlaProGlySerGlyTyr	80
Db	181	CCCTGCGGACCGGACCCAGGCGCGAGATGAAGGGGGGGGGCCAGGCCCGGGCGAGCGCAC	240
Qy	81	ArgGlnValPheSerMetAlaAlaMetAsnLysGluGlyTyrThrAlaSerValAlaThr	100
Db	241	CGCCAGGTGTCTTCATGCGCAGCATGAACAAGAAAGGGGAAACAGCTTCGTGTGCACC	300
Qy	101	GlyProAspSerProSerProValProLeuProGluProGlyLysProAlaLeuProGlyAla	120

Db 301 GGGCCAGACTCCCGTCCCGGTGCTTTGGCCCCAGGCGAACAAGCCCTACCTGGGGCC 360

Cy 121 AspGlyThrProPheGlyCysProProGlyArgIlysIlysProSerAspProValIlu 140

Db 361 GACGGAGACCCCTTGGCTGTCTCTCCCGGCGCAAGAAAGCCATCGATCCCGTCAG 420

Cy 141 TrpThrValMetAspValValGluThrPheThrGluIAspIleProGluGlnAlaThr 160

Db 421 TGGACCGAGATGGAGTGTGTGCAATATTTTACGTGAGCTCGATTTCCGAGAGGCGCA 480

Cy 161 AlaPheGlnIluGlnIluIleAspGlyIysSerIleLeuIleMetGlnArgThrAspVal 180

Db 481 GCTTTCCAGAAGACAGAAATTGATGCGAAATTTTGGCTGCTCATGCAAGCGACAGATGTG 540

Cy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuIysIleIleGluHisIleIleIys 200

Db 541 CTCACCGGCGCTGTCATCCGCTCCGGCGCAGCCCTGAAAAATCTAGACACACCATCATAG 600

Cy 201 ValIleuGlnIluIleHisPheGluAspAspAspProAspGlyPheLeuGly 217

Db 601 GTGCTTAGCAAGGCCACTTTGAGGATATGACCCCGATGGCTTTTAGGC 651

RESULT 6  
BD056449

LOCUS	1508 bp	DNA	linear	PAT 27-AUG-2002
DEFINITION	Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis.			

ACCESSION ED056449.1 GI:22602055  
 VERSION ED056449.1  
 KEYWORDS JP 2001506983-A/7.  
 SOURCE Aegudrea victoria

ORGANISM  
Aequorea victoria  
Aequorea Metacosa; Cnidaria; Hydrozoa; Hydrozoa; Leptomedusae;  
Aequoreidae; Aequorea.

**REFERENCE**  
1 (Dates 1 to 1208)  
**AUTHORS** Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
**TITLE** Novel low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
**JOURNAL** Patent: JP 2001506963-A 7 29-MAY-2001;

COMMENT  
BOSTON HEART FOUNDATION INC  
PN JP 2001506983-A/7  
PD 29-MAY-2001

PF	26-NOV-1997	JP	19958524870		
PR	27-NOV-1996	US	60/031330, 03-JUN-1997	US	60/048547
ANN	M LEEB, ROBERT S	LEES, SIMON W	LAW, ANBAL A	ARJONA	PC
A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC					
C07H21/00					
PC	C07K1/00, C07K4/705, C12N5/12, C12Q1/02, C12Q1/68, G01N33/566	CC			
Scrandness:	Single;				
CC	Topology:	Linear;			
FH	Key	Location/Qualifiers.			

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Score:	1170.00
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Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	6
Length:	1208
Matches:	217
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

[illegible]

Oy	2	AspAspValSerGluGluSerGluValProGluSerAspArgProAlaGluAlaHis	40
Db	61	GATGATGTGTCAAGAGGGCTGTGAAGTGGCCGAAGTACCTCTCGAGGGTGGCCAGCAC	120
Oy	41	HisGluLeuAsnGlyGluIuArglyProGluSerAlaIylsGlyIuArgValIylsGluTTPThr	60
Db	121	CACCACTTAAAGGGGAGGGGAGGACTCAGAGTCCAAAGAGAGGTCAAGAGAGTGGACC	180
Oy	61	ProCysGlyProHisGlnGlyGluAspGluIylArgGlyProAlaPProGlySerGlyThr	80
Db	181	CCTGTGGGACCGCACCAAGGCCAGGATAAAGGGCGGCGCCAGGCCCGGGCACCGGCACC	240
Oy	81	ArgGlnValPheSerMetAlaAlaMetCysIylsGluIylGlyThrAlaSerValAlaIthr	100
Db	241	CGCAGAGTGTTCATGATGGCAGCCATGAACAAGAAAGGGGAAACAGTTGTGGTCACC	300
Oy	101	GlyProAspSerProSerProValPProIuLeuProProGlyIylsProAlaLeuProGlyAla	120
Db	301	GGGCCAGATCTCCCGTCCCGCTGGCTTTGGCCCCCAGCAAAACAGCCCTCACTCGGGGCC	360
Oy	121	AspGlyThrProPheGlyCysProPProGlyIylArgIylsGlyIylsProSerAspProValGlu	140
Db	361	GAGGGAGACCCCTTTGGCTGTCTCCCGGGGCAAAAGAAGCATCTGTATCCCGTCGAG	420

141 TrpThrValMetaspValValGluTyrPheThrGluValGluPheProGluGlnIaThr 160

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QY 182 LeuThrGlyLeuSerLeaArgLeuGlyProAlaLeuYstIeTyGluHisHisIleYs 200  
 Db 541 CTACCGGCTGTTCATCCGCCCTGGGGCAGCCCTGAAATCTACGAGACACACATCAAG 600

Qy 201 ValLeuGInGInGIYHIsbheGInuSpAspAspProAspGIyPheLeuGIy 217  
Db 601 GTCCTCAGCAAGGCCACTTCGAGATATGACCCCAATGGCTTCTTAGGC 651

BC030129	1470 bp	mRNA	linear	PRI 16-SEP-200
LOCUS				
BC030129				
RESULT 7				

**DEFINITION** Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone IMAGE:3943601), partial cds.

ACCESSION	BC030129	
VERSION	BC030129.2	GI:33871478
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE

AUTHORS

Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schler, G.D., Altshul, S., Zeeberg, B., Butten, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Martins, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldi, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Udell, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loughell, N.A., Peters, G.J., Abramson, R.D., Mollaly, S.J., Bosak, S.A., McMan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.D., Hultys, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Keltman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shavchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Gilmwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalski, U., Smallos, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE

human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 MEDLINE 22388257  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 1470)  
 AUTHORS Strausberg R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-May-2002) National Institutes of Health, Mammalian



ORIGIN /mol\_type="genomic DNA"

## Alignment Scores:

Pred. No.: 2,34e-54 Length: 1614  
Score: 1170.00 Matches: 217  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-7 (1-217) x AR409337 (1-1614)

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DB 964 GAAAGCGAGTACTTGAGAAAGAGAGAGAGAGATGATGATGAAGATGAAGATGAAGAA 1023  
QY 21 ASPAPVALSERGLUGLUSERGLUVALPROGLUSERASPAPPROVALAGLVALAGLHIS 40  
DB 1024 GATGATGTGTCAAGAGGCTCTGAAGTCCCGAGAGTGAACCTCTGCAAGTCCCAAGC 1083  
QY 41 HISGLLEUAANGLYLUARGLYLPROGLINERLALYSGLUARGVALLYSGLUPTPTHR 60  
DB 1084 CACACAGCTTAACGGCGAGCGAGCGGAGCCTCAGAGTCCCAAGAGAGAGGTCAAGAGTGAACC 1143  
QY 61 PROCYSGLYPROHISGLINGLYGLINASPGLUGLUGLUGLUAAPSPAPGLUAAPGLUGLU 80  
DB 1144 CCGTCCGAGCGCAGCCAGGCGCAGATGAAGGCGCGGCGCCAGCGCGGCGAGCGGAGCC 1203  
QY 81 ARGGLNVALPHESEMERLALAMETASNLVSGLYGLYTHRALSERVALALATHR 100  
DB 1204 CGCCAGGTGTTCTCCATGSCAGCCATGAACAGAGAGAGGAGGAGACGTTCTGTGCCACC 1263  
QY 101 GLYPROASPSETPROSETPROVALPROLEUPROPROGLYLYSPROALALEUPROGLYALA 120  
DB 1264 GGGCGAGACTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCG 1323  
QY 121 ASPGLYTHRPROPHGLCYSPROPROGLYLYSPROGLYLYSPROSETPROVALAGLU 140  
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QY 141 TRYTHRVALMETASPVVALGLUTYRPHETHRGLUALAGLYPHEPROGLUGLINALATHR 160  
DB 1384 TGGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1443  
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QY 201 VALLEUGLINGLUGLULYSPHEGLUASPAPSPAPSPAPSPAPSPAPSPAPSPAPSPAP 217  
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LOCUS AX239602  
DEFINITION Sequence 45 from Patent WO0164874.  
ACCESSION AX239602  
VERSION AX239602.1 GI:15797275  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
TITLE Low density lipoprotein binding proteins and their use in diagnosing  
and treating atherosclerosis  
JOURNAL Patent: WO 0164874-A 45 07-SEP-2001;

FEATURES Boston Heart Foundation, Inc. (US)  
Location/Qualifiers  
1. 1614  
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1. 1614  
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## ORIGIN

## Alignment Scores:

Pred. No.: 2,34e-54 Length: 1614  
Score: 1170.00 Matches: 217  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

US-09-976-740-7 (1-217) x AX239602 (1-1614)

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DB 1024 GATGATGTGTCAAGAGGCTCTGAAGTCCCGAGAGTGAACCTCTGCAAGTCCCAAGC 1083  
QY 41 HISGLLEUAANGLYLUARGLYLPROGLINERLALYSGLUARGVALLYSGLUPTPTHR 60  
DB 1084 CACACAGCTTAACGGCGAGCGAGCGGAGCCTCAGAGTCCCAAGAGAGAGGTCAAGAGTGAACC 1143  
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QY 81 ARGGLNVALPHESEMERLALAMETASNLVSGLYGLYTHRALSERVALALATHR 100  
DB 1204 CGCCAGGTGTTCTCCATGSCAGCCATGAACAGAGAGAGGAGGAGACGTTCTGTGCCACC 1263  
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DB 1384 TGGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1443  
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DB 1444 GCTTCCAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1503  
QY 181 LEUTHRGLYLEUSERLEIARGLEUGLYPROALALEUYSILEYRGUWHISHSILELS 200  
DB 1504 CTCACCGGCTGTCCATCCGCTCGGGCGAGCCCTGAAAATCTACGAGCAACCATCAAG 1563

QY 201 ValLeuGlnGlnGlyHisPheGluAspAspProAspGlyPheLeuGly 217  
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 DEFINITION AY453840  
 VERSION AY453840.1 GI:38565528  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1617)  
 Lees, A.M., Deconinck, A.E., Campbell, B.D. and Lees, R.S.  
 Atherin, a newly identified LDL-binding protein in human  
 atherosclerotic lesions  
 Unpublished  
 2 (bases 1 to 1617)  
 Deconinck, A.E., Law, S.W., Lees, R.S. and Lees, A.M.  
 Submitted (30-OCT-2003) Harvard-MIT Division of Health Sciences and  
 Technology, Boston Heart Foundation, 139 Main Street, Cambridge, MA  
 02142, USA

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 Best Local Similarity: 100.00% Mismatches: 0  
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 US-09-976-740-7 (1-217) x AY453840 (1-1617)

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QY 21 AspAspValSerGlnGlySerGlnValProGlnSerAspArgProAlaGlnHis 40  
 Db 1024 GATGATGTGTCAAGGGCTCTGAGTCCCGAGAGTGAACCGTCTCAGGTGCCGAC 1083

QY 41 HisGlnLeuAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60

Db 1084 CACACGCTTAAAGCGGAGCGGGGACCTCAGAGTCCAGAGAGAGGTCAGAGTGGAC 1143  
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 Db 1144 CCTGCGGACCGGACCGAGCGGCGGAGTGAAGAGCGGCGGCGGCGGCGGCGGAC 1203

QY 81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlnGlnGlnGlnGlnGlnGln 100  
 Db 1204 CGCCAGGTTGTTCTCATTGAGGAGCCATGAAAGAGAGAGAGAGAGAGAGAGAG 1263

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 Db 1264 GGGCAGACCTCCCGTCCCGGCTGCTTCCCGGCGGCGGCGGCGGCGGCGGCGG 1323

QY 121 AspGlyThrProPheGlyCysProProGlyArgLysGlnGlnGlnGlnGlnGlnGln 140  
 Db 1324 GACGAGACCCCTTGGCTGTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1383

QY 141 TrpThrValMetAspValAlaGlnGlyPheThrGlnGlnGlnGlnGlnGlnGln 160  
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 Db 1504 CTCACCGGCTGTCTCATCCCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1563

QY 201 ValLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 217  
 Db 1564 GTGCTTCAGCAGGACCTTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1614

RESULT 11  
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 DEFINITION ARI99531  
 ACCESSION ARI99531  
 VERSION ARI99531.1 GI:20249605  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 1362)  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis  
 Patent: US 6355451-A 12 12-MAR-2002;  
 Location/Qualifiers  
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 Best Local Similarity: 88.64% Mismatches: 7  
 Query Match: 89.53% Indels: 3  
 Gaps: 2  
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 US-09-976-740-7 (1-217) x ARI99531 (1-1362)

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QY 21 AspAsp-----ValSerGlnGlySerGlnValProGlnSerAspArgProAlaGln 38  
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QY 39 GlnHisIshIsgIleuAen---GlyGluArgGlyProGlnSerAlaIysGluArgValIys 57  
 DB 157 CAGATACACCACTGAAATGCGGAGCGAGCCCGCAGACCGCAAGAGCGGCCAG 216  
 QY 58 GluTrpThrProCysGlyProHisIsgIleuAenGluArgGlyProAlaProGly 77  
 DB 217 GAGTGTGCTGTGTGGCCCGCCACCTGGCCAGAGAAAGGCGGGGCCGCCGCCG 276  
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 DB 277 AGTGGACCCGCGCGAGTGTCTCCATGCGCGCTTGAGTAAAGAGGCGGATCAGCTCT 336  
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 DB 337 TCGACCAACCGGCTGACTCCCGCTCCCGGCTTGGCCCGCCGAGAGCCAGCCCTC 396  
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 DB 457 CCCGTGAGTGAAGACATGACGTGTGAGTACTTCAACGAGCGGCGCTTCCCTGAG 516  
 QY 158 GlnAlaThrAlaPheGlnGluGlnIleAspGlyIysSerLeuLeuMetGlnArg 177  
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 QY 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuIleIleArgIleHis 197  
 DB 577 ACCGATGTCTCATCCGCGCTGTCCATCGCTGGCGCACGCTTGAATCTATGAGCAC 636  
 QY 198 HisIleIysValLeuGlnGlnIleIlePheGluAspAspProAspGlyPheLeuGly 217  
 DB 637 CATATCAAGTGTGCGACGAGGTCACTTCCAGAGACATACCCCGAAGGCTTCTTGGA 696

RESULT 12  
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 DEFINITION Sequence 12 from patent US 6605588.  
 ACCESSION AR374683  
 VERSION AR374683.1 GI:40077498  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1362)  
 AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
 TITLE Low density lipoprotein binding proteins and their use in  
 JOURNAL Patent: US 6605588-A 12 12-AUG-2003;  
 FEATUERS location/Qualifiers  
 source 1. 1362  
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 QY 21 AspAsp-----ValSerGluGlySerGluValProGluSerAspArgProAlaGlyAla 38

DB 97 GACGACGACGTGTGTCTCCAGAGGCTCGAGAGGCGCCGAGAGATGCTCCGCGGATGG 156  
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 QY 198 HisIleIysValLeuGlnGlnIleIlePheGluAspAspProAspGlyPheLeuGly 217  
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 ACCESSION AR409318  
 VERSION AR409318.1 GI:40160106  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1362)  
 AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
 TITLE Low density lipoprotein binding proteins and their use in  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,086-48 Length: 1362  
 Score: 1047.50 Matches: 195  
 Percent Similarity: 95.45% Conservative: 15  
 Best Local Similarity: 88.64% Mismatches: 7  
 Query Match: 89.53% Indels: 3  
 DB: 6 Gaps: 2

US-09-976-740-7 (1-217) x AR409318 (1-1362)

QY 1 GluGluArgValIleuGluIysGluGluGluAspAspGluAspGluAspGluGlu 20  
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Parent: JP 2001506983-A 3 29-MAY-2001;

BOSTON HERPETO FOUNDATION INC

PN JP 2001506983-A/3

PD 29-MAY-2001

PR 26-NOV-1997 JP 1998524870

PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI

ANN M LEES, ROBERT S LEES, SIMON W LAM, ANIBAL A ARJONA PC

A6IK38/04, A6IK38/17, A6IK39/00, A6IK48/00, A6IK49/00, A6IK51/08, PC

C07H21/00

PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC

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CC Topology: Linear;

FH Key Location/Qualifiers.

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Location/Qualifiers  
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## ORIGIN

## Alignment Scores:

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Percent Similarity:	95.45%	Conservative:	15
Best Local Similarity:	88.64%	Mismatches:	7
Query Match:	89.53%	Indels:	3
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US-09-976-740-7 (1-217) x BD056445 (1-1362)

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QY      39  GluHisHisGluLeuAsn--GlyGluArgGlyProGluSerAlaLysGluArgValLys 57
Db     157  CAGCATCAGCAGCTGGAATGGCGGAGCGGCGCCGACGCGCCGACGCGGAGAGAGAGAG 216
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QY     158  GluAlaThrAlaPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 177
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QY     178  ThrAspValLeuThrGlyLeuSerLeuArgLeuGlyProAlaLeuLysIleTyrgLHis 197
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Job time : 3305.9 secs



Mon Mar 15 09:28:17 2004

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Page 1

GenCore version 5.1.6  
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Run on: March 12, 2004, 20:05:17 ; Search time 73.5728 Seconds

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Perfect score: 1170

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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

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Maximum Match 100%  
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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5	1047.5	89.5	1362	4	US-08-979-608A-12
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7	1047.5	89.5	1362	4	US-09-616-289-12
8	1047.5	89.5	1422	4	US-08-979-608A-13
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13	1047.5	89.5	1617	4	US-09-616-289-11	Sequence 11, Appl
14	1047.5	89.5	2561	4	US-09-616-289-48	Sequence 48, Appl
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16	390	33.3	1425	4	US-09-621-976-9791	Sequence 9791, Ap
17	285	24.4	1453	4	US-09-976-594-760	Sequence 760, App
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19	168.5	14.4	1933	3	US-08-974-380-1	Sequence 1, Appl
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22	154.5	13.2	3065	2	US-08-852-153-7	Sequence 7, Appl
23	153	13.1	3879	3	US-08-916-352-1	Sequence 1, Appl
24	144	12.3	2855	2	US-08-852-153-1	Sequence 1, Appl
25	144	12.3	3255	2	US-08-852-153-5	Sequence 5, Appl
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#### ALIGNMENTS

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Sequence 16, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIORITY DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/559818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..651  
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Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
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FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-8906  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-517-849-16  
Alignment Scores:  
Pred. No.: 1,34e-86 Length: 1208  
Score: 1170.00 Matches: 217  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
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DB 181 CCTCGGAGCGGAGCGGCGGAGGATGAAGGCGGCGGCGGAGCGGCGGCGGAGCACC 240





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1 STREET: 225 Franklin Street
2 CITY: Boston
3 STATE: MA
4 COUNTRY: USA
5 ZIP: 02110-2804
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Diskette
9 COMPUTER: IBM Compatible
10 OPERATING SYSTEM: DOS
11 SOFTWARE: FastSeq for Windows Version 2.0
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13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/979,608A
15 FILING DATE: 26-NOV-1997
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17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 60/048,547
19 FILING DATE: 03-JUN-1997
20 APPLICATION NUMBER: US 60/031,930
21 FILING DATE: 27-NOV-1996
22
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Myers, Louis
25 REGISTRATION NUMBER: 35,965
26 REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3583/59818)
27
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 617/542-5070
30 TELEFAX: 617/542-8906
31
32 INFORMATION FOR SEQ ID NO: 12:
33
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 1362 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
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42 LOCATION: 1...696
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; SOFTWARE: FastSeq for Windows Version 4.0

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (656)
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US-09-616-289-12

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Percent Similarity:	95.45%	Conservative: 15
Best local Similarity:	88.64%	Mismatches: 7
Query Match:	89.53%	Indels: 3
DB:	4	Gaps: 2

US-09-976-740-7 (1-217) X US-09-616-289-12 (1-1362)

[illegible]

RESULT 8  
US-08-979-608A-13  
; Sequence 13, Application US/08979608A  
; Patent No. 6355451  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; Lees, Robert S.  
; Law, Simon M.  
; Ajlona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C  
STREET: 225 Franklin Street  
CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02110-2

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compati

OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:

FILING DATE: 26-NO. 6355451-1997  
PRIOR APPLICATION DATA:

FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996

NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (former) v 3983/59818

TELECOMMUNICATION INFORMATION  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906

SEQUENCE CHARACTERISTICS:  
LENGTH: 1422 base pairs  
TYPE: nucleic acid

TOPOLOGY: linear  
FEATURE:

LOCATION: 1..756  
SEQUENCE DESCRIPTION: SEQ ID NO: 13  
9-608A-13

Length:	1422
Matches:	195
Conservative:	15
Mismatches:	7
Indels:	3
Gaps:	2

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217 CACATCATCACAGCTGAATGCGCGAGCGCGCGCGCGACCGCCAGACCGACGAGCGGACG 278  
58 GluTrpThrProCysGlyProHisGlnGlyGlnAspGluGlyArgGlyProAlaProGly 77  
277 GAGTGTGCTGTGTGTGGCCCGCACCTGGCCAGAGGAAGGGCGGGGCGCGCGGGAC 336  
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337 AGTGGACACCGCGAGGTGTCTTCATGGCGGGCTTGAATTAAGAGAGGGGGATCGACCTCT 396





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Db AGTGCACCCCGGAGTCTTCATGCGGCTTGAGTAAGAGGGGGGATCAGCCTCT 591  
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## RESULT 12

US-09-517-849-11  
; Sequence 11, Application US/09517849  
; Patent No. 6605588

## GENERAL INFORMATION:

APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.

Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Fish & Richardson P. C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/517, 849

FILING DATE: 02-Mar-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979, 608

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35, 965

REFERENCE/DOCKET NUMBER: 10797-003001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1617 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Alignment Scores:  
Pred. No.: 1,816-76 Length: 1617  
Score: 1047.50 Matches: 195  
Percent Similarity: 95.45 Conservative: 15  
Best Local Similarity: 88.648  
Query Match: 89.538 Indels: 3  
DB: 4 Gaps: 2

US-09-976-740-7 (1-217) x US-09-517-849-11 (1-1617)

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Db 352 GACGACGAGTGTGTCCGAGGCTCGAGGTGCGCCGAGAGCGATGCTCCCGGGTGGC 411  
Qy 39 GlnHisGlnLeuAsn---GlyGluArgGlyProGlnSerAlaGlyGluGlyValys 57  
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## RESULT 13

US-09-516-289-11  
; Sequence 11, Application US/09616289  
; Patent No. 6632923

## GENERAL INFORMATION:

APPLICANT: Lees, Ann M.

APPLICANT: Lees, Robert S.

APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

TITLE OF INVENTION: ATHEROSCLEROSIS

FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/616, 289

CURRENT FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 09/517, 849

PRIOR FILING DATE: 2000-03-02

PRIOR APPLICATION NUMBER: US 08/979, 608









Mon Mar 15 09:28:18 2004

us-09-976-740-7.rnpb

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Run on: March 12, 2004, 20:46:42 ; Search time 313.946 Seconds  
(without alignments)  
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Fgapop 6.0 , Fgapext 7.0  
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Searched: 2432557 seqs, 1840798884 residues

Total number of hits satisfying chosen parameters: 4865114

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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7	1170	100.0	1208	15	US-10-616-187-16	Sequence 16, Appl
8	1170	100.0	1445	10	US-09-945-527-6	Sequence 6, Appl
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## ALIGNMENTS

RESULT 1  
US-09-962-055-16  
; Sequence 16, Application US/09962055  
; Patent No. US20020052033A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Lee, Robert S.  
Arlona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/962,055  
 FILING DATE: 24-Sep-2001

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/979,608  
 FILING DATE: 26-NOV-1997  
 APPLICATION NUMBER: US 60/031,930  
 FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Myers, Louis  
 REGISTRATION NUMBER: 35,965  
 REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1208 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 1...651  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-962-055-16

Alignment Scores:  
 Pred. No.: 2,386-99 Length: 1208  
 Score: 1170.00 Matches: 217  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-7 (1-217) x US-09-962-055-16 (1-1208)

```

QY      1  GluGluArgValLeuGluLysGluGluGluAspAspAspGluAspGluGlu 20
DB      1  GAAGAGCGAGTACTTGAGAAAGAGAGAGAGAGATGATGATGAAGTGAAGAA 60
QY      21  AspAspValSerGluGluSerGluValProGluSerAspArgProAlaGluHis 40
DB      61  GATGATGTGTCAAGAGGGCTCTGAAGTGCCTGAGAGTGAAGTGCCTGAGTGC 120
QY      41  HisGluLeuAsnGluGluArgGlyProGluSerAlaGluGluArgValLysGlu 60
DB      121  CACGAGCTTAACGGCGAGCGGGAGCTCAGAGTCCCAAGAGAGGGTCAAGAG 180
QY      61  ProCysGlyProHisGlnGluGluAspGluGlyArgGlyProAlaProGlySerG 80
DB      181  CCTGCGGAGCCGACCGAGCGGCGGATGAAGCGGCGGCGGCGGCGGCGGCGGCG 240
QY      81  ArgGluValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerVal 100
DB      241  CGCAGAGTGTTCACAGGACGACGATGAACAGAGAGGGGAGACAGCTTCTGTC 300
QY      101  GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuPro 120
DB      301  GGGCGACACTCCCGCTCCCGGCGCTTTCCTCCCGGCGCAACAGCCCTACCTG 360
QY      121  AspGlyThrProPheGlyCysProProGlyValArgLysGluLysProSerAsp 140
DB      361  GACCGGAGCCCGCTTGGCTGTCTCCCGGCGCAAGAGAGCCATCTGATCCGTC 420
QY      141  ThrThrValMetAspValAlaGluLysPheThrGluAlaGlyPheProGluGln 160
DB      421  TGGACCTGATGATGTCTGTGAATATTTTACTGAGGCTGATTTCCCGAGGAGCA 480
QY      161  AlaPheGlnGluGlnGluLysAspGlyLysSerLeuLeuLeuMetGlnArgThr 180
DB      481  GCCTTCAAGAGCGAGAAATGATGAGCAAACTTTGCTGCTCATGACGCGCAAG 540
  
```

RESULT 2

US-09-976-740-16

Sequence 16, Application US/09976740  
 Publication No. US20020194633A1

GENERAL INFORMATION:  
 APPLICANT: Lees, Ann M.  
 APPLICANT: Lees, Robert S.  
 APPLICANT: Lay, Simon W.  
 APPLICANT: Aijona, Anibal A.  
 TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
 TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
 TITLE OF INVENTION: ATHEROSCLEROSIS  
 FILE REFERENCE: 10797-004001

CURRENT APPLICATION NUMBER: US/09/976,740  
 CURRENT FILING DATE: 2001-10-12  
 PRIOR APPLICATION NUMBER: 09/616,289  
 PRIOR FILING DATE: 2000-07-14  
 PRIOR APPLICATION NUMBER: US 08/979,608  
 PRIOR FILING DATE: 1997-11-26  
 PRIOR APPLICATION NUMBER: US 60/031,930  
 PRIOR FILING DATE: 1996-11-27  
 PRIOR APPLICATION NUMBER: US 60/048,547  
 PRIOR FILING DATE: 1997-06-03  
 NUMBER OF SEQ ID NOS: 53  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 16

LENGTH: 1208  
 TYPE: DNA  
 ORGANISM: Homo sapiens

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)...(651)

US-09-976-740-16

Alignment Scores:  
 Pred. No.: 2,386-99 Length: 1208  
 Score: 1170.00 Matches: 217  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-7 (1-217) x US-09-976-740-16 (1-1208)

```

QY      1  GluGluArgValLeuGluLysGluGluGluAspAspAspGluAspGluGlu 20
DB      1  GAAGAGCGAGTACTTGAGAAAGAGAGAGAGATGATGATGAAGTGAAGAA 60
QY      21  AspAspValSerGluGluSerGluValProGluSerAspArgProAlaGluHis 40
DB      61  GATGATGTGTCAAGAGGGCTCTGAAGTGCCTGAGAGTGAAGTGCCTGAGTGC 120
QY      41  HisGluLeuAsnGluGluArgGlyProGluSerAlaGluGluArgValLysGlu 60
DB      121  CACGAGCTTAACGGCGAGCGGGAGCTCAGAGTCCCAAGAGAGGGTCAAGAG 180
QY      61  ProCysGlyProHisGlnGluGluAspGluGlyArgGlyProAlaProGlySerG 80
DB      181  CCTGCGGAGCCGACCGAGCGGCGGATGAAGCGGCGGCGGCGGCGGCGGCGGCG 240
QY      81  ArgGluValPheSerMetAlaAlaMetAsnLysGluGlyGlyThrAlaSerVal 100
DB      241  CGCAGAGTGTTCACAGGACGACGATGAACAGAGAGGGGAGACAGCTTCTGTC 300
  
```



[illegible]



```
Db 546 GAGGAGACCCCTTGTGCTGCTCCCGGCGGCAAGAGACATCTGATCCCGTCGAG 605
Qy 141 TPTThValMeKaspValValGluTyrPheThrGluAlaGlyPheProGluGlnAlaThr 160
Db 606 TGGACCGTGAATGATGATGCGCAATATTTTACGAGGCTGGATCCCGAGAGAGCGGACA 665
Qy 161 AlAphGlnGlnGlnGlnIleAaspGlyLysSerLeuLeuMetGlnThrAspVal 180
Db 666 GCTTCCAGAGACAGAAATGATGACCAATCTTCTGCTCATGAGCGACAGATGTG 725
Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLys 200
Db 726 CTCACCGGCTGTCTCCATCCGCTCCGCGGACGCTTAAATCTTACAGACACACATCAG 785
Qy 201 ValLeuGlnGlnGlnIleHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db 786 GTGCTTCAGCAGGACCACTTGAAGATGATGACCCGATGCTTCTTACGC 836

RESULT 8
US-09-976-740-45
; Sequence 45, Application US/09976740
; Publication No. US20020194633A1
GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/09/976, 740
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/616, 289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/979, 608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031, 930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048, 547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-09-976-740-45

Alignment Scores:
Pred. No.: 3,25e-99 Length: 1614
Score: 1170.00 Matches: 217
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-976-740-7 (1-217) x US-09-976-740-45 (1-1614)
Qy 1 GluGluArgValLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 20
Db 964 GAAAGAGCGAATCTTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 1023
Qy 21 AspAspValSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
Db 1024 GATGATGTGTCAAGAGGCGCTCTGAAGTGCAGAGAGTGCAGGCTCTGAGGTCAGCAC 1083
Qy 41 HisGlnLeuAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60
```

```
Db 1084 CACCACTTAACGGCGAGCGGAGCCTCAGAGTGCACAGAGAGAGGTCAGAGTGCAGC 1143
Qy 61 ProCysGlyProHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 80
Db 1144 CCGCGCGAGCCGACACAGGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1203
Qy 81 ArgGlnValPheSerMetAlaAlaMetAsnLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
Db 1204 CGCCAGGAGTGTCTCCATGAGGAGCCATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1263
Qy 101 GlyProAspSerProSerProValProLeuProGlnProGlnProGlnProGlnProGln 120
Db 1264 GGGCCAGACTCCCGTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCG 1323
Qy 121 AspGlyThrProPheGlyCysProProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
Db 1324 GACGAGACCCCTTGGCTGTCCGCGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383
Qy 141 ThrThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGlnGlnAlaThr 160
Db 1384 TGGACCGTGAATGATGATGCGCAATATTTTACGAGGCTGGATCCCGAGAGAGCGGACA 1443
Qy 161 AlAphGlnGlnGlnGlnIleAaspGlyLysSerLeuLeuMetGlnThrAspVal 180
Db 1444 GCTTCCAGAGACAGAAATGATGACCAATCTTCTGCTCATGAGCGACAGATGTG 1503
Qy 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLys 200
Db 1504 CTCACCGGCTGTCTCCATCCGCTCCGCGGACGCTTAAATCTTACAGACACACATCAG 1563
Qy 201 ValLeuGlnGlnGlnIleHisPheGluAspAspAspProAspGlyPheLeuGly 217
Db 1564 GTGCTTCAGCAGGACCACTTGAAGATGATGACCCGATGCTTCTTACGC 1614

RESULT 9
US-10-671-242-45
; Sequence 45, Application US/10671242
; Publication No. US20040040049A1
GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/671, 242
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US/09/616, 289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517, 849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979, 608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031, 930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048, 547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1614)
US-10-671-242-45

Alignment Scores:
Pred. No.: 3,25e-99 Length: 1614
Score: 1170.00 Matches: 217
```



Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-976-740-7 (1-217) X US-10-671-242-45 (1-1614)

QY	1	GlucutArvValLeuGIuLySGIuGIuGIuGIuLysAspAspArgLysArgLysGIu	20
Db	964	GAAGGCGAGTACTTGAAGAAAGAGGAGAAGATGATGTGAAGATGAAGATGAAGA	1023
QY	21	AspAspValSerGIuGIuSerGIuValProGIuSerAspArgProAlaGIuAlaHis	40
Db	1024	GATATGTGTAGAGGGCTGTGAAGTGGCCAGAGTGACCGCTCTGCAGGGTGCCAGAC	1083
QY	41	HisGluLeuAsnGIuGIuArgGIuProGlnSerAlaLysGIuArgValLysGIuTrpThr	60
Db	1084	CACCAAGCTTAACGGGAGACGGGGACCTCAGAGTGCACAGAGAGGTCAAGAGTGGACC	1143
QY	61	ProCysGIuProHisGIuGIuGIuAspGIuGIuArgGIuProAlaProGIuSerGIuThr	80
Db	1144	CCCTGGGAGCCGACACAGGCCAGGATAGAGGGCGGGGGCCAGGCCCGGGAGCGGGACC	1203
QY	81	ArgGIuValPheSerMetAlaAlaMetAsnLysGIuGIuGIuTrpAlaSerValAlaThr	100
Db	1204	CGCCAGGGTGTCTCCATGCGACCATGAAACAAGAGGGGAGAACAGCTTCTGTGGCCAC	1263
QY	101	GIuProAspSerProSerProValProLeuProProGIuLysProAlaLeuProGIuAla	120
Db	1264	GGGCGAGCTCCCGCTCCCGCTGCTTGGCCCCCAGCAACAGCCCTTACTGGGGCC	1323
QY	121	AspGIuThrProPheGIuCysProProGIuArgLysGIuLysProSerAspProValGIu	140
Db	1324	GACGGGACCCCTTGGCTGTCTCGGCCGGGGCAAGAGGACCATCTGAATCCGTCGAG	1383
QY	141	TrpThrValMetAspValValGIuTrpPheThrGluAlaGIuPheProGIuAlaAlaThr	160
Db	1384	TGGAACCGTGATGGATGTCTGGAATATTTCCTAGAGCTGATATTCGGAGACAGGCACA	1443
QY	161	AlaPheGlnGIuGIuGIuIleAspGIuLysSerIleuLeuMetGlnArgThrAspVal	180
Db	1444	GCTTTCACAAGGACGAGAAATTGAATGGCAAACTTGTGCTCAAGACAGGACAGATGTG	1503
QY	181	LeuThrGIuLysSerIleArgLeuGIuProAlaLeuLysIleTyrGIuHisHisIleLys	200
Db	1504	CTCAACGGGCTGTGCATCCGCTCGGGGCAAGCCCTGAAATATCTAGAGACACCATCAAG	1563
QY	201	ValLeuGlnGIuGIuHisPheGluAspAspAspProAspArgIlePheLeuGIu	217
Db	1564	GTGCTTCGCAAGGCCACTTGAAGATGATACCCCAATGGCTCTTAAAGC	1614

**RESULT 10**

Sequence 45, Application US/10023529  
Publication No. US20020129388A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon M.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930

```

PRIORITY FILING DATE: 1996-11-27
PRIORITY APPLICATION NUMBER: US 60/048,547
PRIORITY FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1614)
US-10-023-529-45

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### Alignment Scores

Pred. No.:	3,25e+99	Length:	161
Score:	1170.00	Matches:	217
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
B3:	13	Gaps:	0

US-09-976-740-7 (1-217) X US-10-023-529-45 (1-1614)

[illegible]

## RESULT 11

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US-10-023-523-45
; Sequence 45, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
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Qy 138 ProValGluTrpThrValMetAspValValGluTyrPheThrGluIleGlyPheProGlu 157
Db 457 CCCGTGGAGTGGACAGTCATGGAGTCGTGGAGTACTTCAACGAGGCGGCTTCCCTGAG 516
Qy 158 GlnAlaThrAlaPheGlnGlnGlnGluIleAspGlyLysSerLeuLeuMetGlnArg 177
Db 517 CAAGCCACGGGCTTCCAGAGACAGAGATCGACGGCAAGTCCCTGCTGCTCATGCAAGCGC 576
Qy 178 ThrAspValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHis 197
Db 577 ACCGATGTCTCACCGGCTGTCCATCCGCTGGGGCCAGCGTTGAAATCTATGAGCAC 636
Qy 198 HisIleLysValLeuGlnGlnGlnGlyHisAspGluAspAspProAspGlyPheLeuGly 217
Db 637 CATATCAAGGTGCTGCAGCAGGAGTCACTTCAGAGACGATGACCCGGAAGGCTTCTGGGA 696

```

Search completed: March 13, 2004, 04:26:11  
Job time : 319.946 secs





**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LNCM69 row: h column: 02  
 High quality sequence stop: 749.

**FEATURES****Source**

1. 1109  
 Location/Qualifiers

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2966449"  
 /tissue\_type="Burkitt lymphoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_8"  
 /note="Organ: lymph; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

**ORIGIN****Alignment Scores:**

Pred. No.: 9,296-64 Length: 1109  
 Score: 1170.00 Matches: 217  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0

US-09-976-740-7 (1-217) x BE270805 (1-1109)

QY 1 GluGUUArgValLeuGUUySerGUUgUgUUAAspAspGUUAspGUUAspGUU 20  
 Db 39 GAAGAGCGAGTACTTGAGAAAGAGAGAGAGATGATGATGATGATGATGATGATG 98  
 QY 21 AspAspValSerGUUySerGUUValProGUUySerAspAspProGUUySerGUU 40  
 Db 99 GATGATGTGCAAGGGCTCTGAGATGCGGAGAGTGAACCTCTGAGGTGCCAGCAC 158  
 QY 41 HisGUULeuAnGUUArgGUUyProGUUySerGUUyValGUUySerGUUySerGUU 60  
 Db 159 CACAGCTTAACGGCGAGCGGGAGCTCAGAGTGCAGAGAGAGGGTCAAGAGTGCACC 218  
 QY 61 ProGUUySerGUUySerGUUyValProGUUySerAspAspProGUUySerGUU 80  
 Db 219 CCGTCCGAGCGAGCGAGCGGGAGTGAAGGGCGGGCGAGCGGGCGAGCGGACCC 278  
 QY 81 ArgGUUValPheSerMetAlaAlaMetAspLeuGUUyValGUUySerValAlaThr 100  
 Db 279 CGCCAGGTCTTCTCCATGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 338  
 QY 101 GUYProAspSerProSerProValProLeuProGUUyValGUUySerProGUUy 120  
 Db 339 GGAGCGAGACTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCCCGTCC 398  
 QY 121 AspGUUySerProGUUySerProGUUyValGUUySerProGUUySerProGUUy 140  
 Db 399 GAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 458  
 QY 141 TrpThrValMetAspValValGUUyPheThrGUUyValGUUyPheProGUUyVal 160  
 Db 459 TGAACCGTATGATGTGCGTGAATATTATTTAGAGGTGATGATGATGATGATGATG 518

QY 161 AaPheGUUySerGUUyValGUUySerGUUyValGUUySerGUUyValGUUySerGUU 180  
 Db 519 GCTTCCAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 578  
 QY 181 LeuThrGUUySerGUUyValGUUySerGUUyValGUUySerGUUyValGUUySerGUU 200  
 Db 579 CTCACGGCGCTGCTCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 638  
 QY 201 ValLeuGUUySerGUUyValGUUySerGUUyValGUUySerGUUyValGUUySerGUU 217  
 Db 639 GTGCTTCAAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 689

**FEATURES****Source**

RESULT 2  
 BE561424 858 bp mRNA linear EST 15-AUG-2000  
 LOCUS 601344543p1 NIH\_MGC\_8 Homo sapiens CDNA clone IMAGE:3677194 5'  
 DEFINITION mRNA sequence.  
 ACCESSION BE561424  
 VERSION BE561424.1 GI:9805144  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

**REFERENCE** NIH-MGC <http://mgc.nci.nih.gov/>  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LNCM69 row: f column: 11  
 High quality sequence stop: 709.

**FEATURES****Source**

1. 858  
 Location/Qualifiers

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3677194"  
 /tissue\_type="Burkitt lymphoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_8"  
 /note="Organ: lymph; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

**ORIGIN****Alignment Scores:**

Pred. No.: 3,26-59 Length: 858  
 Score: 1095.50 Matches: 211  
 Percent Similarity: 98.60% Conservative: 0  
 Best Local Similarity: 98.60% Mismatches: 3  
 Query Match: 93.63% Indels: 2  
 Gaps: 0

US-09-976-740-7 (1-217) x BE561424 (1-858)

QY 1 GluGUUArgValLeuGUUySerGUUgUgUUAAspAspGUUAspGUUAspGUU 20  
 Db 38 GAAGAGCGAGTACTTGAGAAAGAGAGAGATGATGATGATGATGATGATGATG 97  
 QY 21 AspAspValSerGUUySerGUUValProGUUySerAspAspProGUUySerGUU 40



```

Db      98  GATGATGTGTCTGAGAGGCTCTGAAGTCCCGAGAGTACCGTCTCGAGGTGCCAGCAC 157
Qy      41  HGGHLEuasmnlygluargylproglinserialyregluargvallysgutptthr 60
Db      158  CACACGCTTACGCGGAGCGGAGCTCAGAGTGCACAGAGAGGCTCAAGAGTGGACC 217
Qy      61  ProCysglYProHISglnglygluaspGLyArgGLYProAlaproglyserGLYthr 80
Db      218  CCTGGCGAGCGGACCA-GGCCAGAGTGAAGGGGGGGCGACCCCGGCGAGCGGAC 276
Qy      81  ArgGlnValPheSerMetAlaAlaMetAsnlysgluGLYglYThrAlaSerValAlaThr 100
Db      277  CGCGAGGTGTCTTCATGAGCGACCATGACACAGAGAGGAGGAGAGCTTCTGTGCCACC 336
Qy      101  GlyProAspSerProSerProValProLeuProglYlysProAlaLeuProGLYAla 120
Db      337  GGGCGAGACTCCCGTCCCGGCTGCTTGGCCCGGCGAGAACAGCCCTACCTGGGGCC 396
Qy      121  AspGLYThrProPheGLYCySPProGLYArgYlysGLYulysProSerAspProValGlu 140
Db      397  GACGGGACCCCTTGGCTGTCTCCCGGCGAGAGAGAGCATCTGATCCCGTGCAG 456
Qy      141  ThrThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGLYAlaThr 160
Db      457  TGGACCGTGAATGATGTCGTGCAATTTACTGAGGCTGATCCCGGAGCGAGCA 516
Qy      161  AlaPheGlnGlnGlnGlnIleAspGLYlysSerLeuLeuMetGlnAlaGlyThrAspVal 180
Db      517  GCTTTCACAGGAGCAAGAAATTGATGCAAACTTGTCTCATGAGCGGCAAGATG 576
Qy      181  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuYsIleTyrGlnHisIleIys 200
Db      577  CTCACCGCGCTGTC--ATCCGCGCTCGGGCGAGCCCTGAATCTACGAGCACCATCAG 634
Qy      201  ValLeuGlnGlnGlnIleHisPheGluAspAspAspProAspGLY 214
Db      635  GTGCTTACGACAGGCCACTTGAAGATGATGACCCCATGT 676

RESULT 3
LOCUS   B1226646              785 bp      mRNA      linear      EST 11-JUL-2001
DEFINITION 602951660F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:5095742 5',
mRNA sequence.
ACCESSION B1226646
VERSION   B1226646.1  GI:14680090
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 785)
          NIH-MGC Htcc://mgs.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: rgs@bbs-rcmail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
          CDNA Library Preparation: Ling Hong/Rubin Laboratory
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: LICM1866 row: h column: 15
          High quality sequence, stop: 785.
          Location/Qualifiers
            1..785
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:5095742"
              /tissue_type="Burkitt lymphoma"

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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_8"
/Note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACTAGAG(G). Size selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
2,026-58	785	214	1082.00	98.62%	98.62%	92.48%	12
							Gaps: 0

US-09-976-740-7 (1-217) x B1226646 (1-785)

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Qy      1  GluGluArgValLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 20
Db      59  GAAAGCGAGATCTTGAAGAAAGAGAGAGAGATGATGAAGATGAGATGAGAA 118
Qy      21  AspAspValSerGluGlySerGluValAlaProGluSerAspArgProAlaGlyAlaGlnHis 40
Db      119  GATGATGTGTCTGAGAGGCTCTGAGAGTGCCTGAGAGTGCCTGAGAGTGCCTGAGAG 178
Qy      41  HisGlnLeuAsnGlnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
Db      179  CACACGCTTACGCGGAGCGGAGGAGCTCAGAGTGCACAGAGAGGCTCAAGAGTGCAGC 238
Qy      61  ProCysglYProHISglnglygluaspGLYArgGLYProAlaProglyserGLYthr 80
Db      239  CCTCGCGAGCGGACAGAGGCGGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 298
Qy      81  ArgGlnValPheSerMetAlaAlaMetAsnlysgluGLYglYThrAlaSerValAlaThr 100
Db      299  CGCCAGGTGTCTTCATGAGCGACCATGACAGAGAGGAGAGAGCTTCTGTGCCACC 358
Qy      101  GlyProAspSerProSerProValProLeuProglYlysProAlaLeuProGLYAla 120
Db      359  GGGCGAGACTCCCGTCCCGGCTGCTTGGCCCCAGGCAAAACCGCTACCTGGGGCC 418
Qy      121  AspGLYThrProPheGLYCySPProGLYArgYlysGLYulysProSerAspProValGlu 140
Db      419  GACGGGAGC-CCCTTGGCTGTCTCCCGGCGAGAGAGAGCCATCTGATCCCGTGCAG 477
Qy      141  ThrThrValMetAspValValGluTyrPheThrGluAlaGlyPheProGLYAlaThr 160
Db      478  TGGACCGTATGATGTCGTCAATTTTACTGAGCTGATTCGCCGAGAGCGAGCA 537
Qy      161  AlaPheGlnGlnGlnGlnIleAspGLYlysSerLeuLeuMetGlnArgThrAspVal 180
Db      538  GCTTTCACAGGAGCAAGAAATTGATGCAAACTTGTCTCATGACAGCGGCAAGATG 597
Qy      181  LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuYsIleTyrGlnHisIleIys 200
Db      598  CTCACCGGCTTCCATCGCTCGGCGAGCGGCTGAAATTTACAGCA-CACATCAAG 656
Qy      201  ValLeuGlnGlnGlnIleHisPheGluAspAspAspProAspGLYPheLeuGly 217
Db      657  GTGCTTACGACAGGCGACATT-GAGATGATGATGCCCATGCTTCTTGGGC 706

RESULT 4
LOCUS   BUI174966              996 bp      mRNA      linear      EST 04-SEP-2002
DEFINITION AGENCOURT 8073899 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6087267
          5', mRNA sequence.
ACCESSION BUI174966
VERSION   BUI174966.1  GI:22688950

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KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 996)  
TITLE NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

FEATURES  
source  
1..996  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6087267"  
/issue\_type="epidermoid carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 102"  
/note="Organ: salivary gland; Vector: pORF7, Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
High quality sequence stop: 592.  
Location/Qualifiers  
row: 3 column: 04  
Plate: LHCW2323

US-09-976-740-7 (1-217) x BU174966 (1-996)

ORIGIN  
Alignment Scores:  
Pred. No.: 1.14e-57 Length: 996  
Score: 1072.00 Matches: 206  
Percent Similarity: 95.85% Conservative: 2  
Best Local Similarity: 94.93% Mismatches: 6  
Query Match: 91.62% Indels: 3  
DB: 13 Gaps: 1

US-09-976-740-7 (1-217) x BU174966 (1-996)

QY 121 AspGlyThrProPheGlyCybProProGlyAryGlyGlyLysProSerAspProValGlu 140  
DB 499 GACGGAGACCCCTTGGCTGTCTCTCCCGGCGCAAGAGACCATGTATCCCGTGCAG 558  
QY 141 TrpThrValMetAspValValGlyTyrPheThrGlnAglYpHeProGlnGlnAlaThr 160  
DB 559 TGCACCGTGTATGATGATGCTCCATATATTACTGAGCGCTGATCCCGGAGCAAGCACA 618  
QY 161 AlaPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 180  
DB 619 GCTTTCAGAAACGAAATGATGCAAACTTCTCTCATGACGCGCAAAATGT 678  
QY 180 lIeuThrGlyLeuSerIleArgLeuGlyProAlaLeuValIleTyrGlnIshisIlely 200  
DB 679 GCTACCGGCGCTGTCCATCCGCGCGCCGCTGAAATCTAGAGACACCCCATCA 738  
QY 200 sValLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 216  
DB 739 GGTCTTCACAGAGGCGCTTGGGATGATGACCCGATGCGCTTCTT 787

RESULT 5  
BM013469 756 bp mRNA linear EST 30-OCT-2001  
LOCUS BM013469  
DEFINITION mRNA sequence.  
ACCESSION BM013469  
VERSION BM013469.1 GI:16527823  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 756)  
TITLE NIH-MGC http://mgi.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov

US-09-976-740-7 (1-217) x BM013469 (1-756)

#### FEATURES

source

1..756  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5415292"  
/issue\_type="mammary adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 87"  
/note="Organ: breast; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally, oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
High quality sequence stop: 752.  
Location/Qualifiers  
row: 3 column: 05  
Plate: LHM12059

ORIGIN  
Alignment Scores:  
Pred. No.: 4.65e-56 Length: 756  
Score: 1044.00 Matches: 197  
Percent Similarity: 99.49% Conservative: 0  
Best Local Similarity: 99.49% Mismatches: 1  
Query Match: 89.23% Indels: 1  
DB: 12 Gaps: 0

US-09-976-740-7 (1-217) x BM013469 (1-756)

QY 20 GluAspAspValSerGluGlySerGluValProGluSerAspArgProAlaGluGln 39  
Db 1 GAAATGATGATGTCAGAGGGCTCTGAAGTGGCCGAGAGTACCGTCTTCAGAGTGGCCAG 60  
QY 40 HisIleGlnLeuAsnGlyGluArgGlyProGlnSerAlaGlyGluValGlyGluTrp 59  
Db 61 CACCAACAGCTTAAAGGAGAGGAGGAGGAGCTCAGAGTCCAAAGAGAGGAGTCAAGAGAGTGG 120  
QY 60 ThrProCysGlyProHisIleGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGly 79  
Db 121 ACCCTCGTGGAGCCGACCA-GGCCAGAGTGAAGAGGGGGGGCCAGCCCGGGGAGAGGGC 179  
QY 80 ThrArgGlnValPheSerMetAlaAlaMetAsnGlyGluGlyGlyThrAlaSerValAla 99  
Db 180 ACCGCGCAGGTTCTCCATGGCAGCCATGAACAAAGAGGGGGAACAGCTTCTGTGGCC 239  
QY 100 ThrGlyProAspSerProSerProValProLeuProGlyProGlyLysProAlaLeuProGly 119  
Db 240 ACCGGGCGAGACTCCCGTCCCGCTGCTTGGCCCGCAGCAACAGCCCTACCTGGG 239  
QY 120 AlaAspGlyThrProPheGlyCysProProGlyArgGlyGlyLysProSerAspProVal 139  
Db 300 GCCACCGGAGACCCCTTGGCTGTCTCCGGGGCGCAAGAGCCATCTGATCCCGTC 359  
QY 140 GluTrpThrValMetAspValValGluTrpPheThrGluValGlyPheProGluGlnAla 159  
Db 360 GAGTGGACCGTGAAGAGTGTGTCGAATATTACTAGAGTGGATTCCCGAGAGAGCG 419  
QY 160 ThrAlaPheGlnGlnGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAsp 179  
Db 420 ACAGCTTCCAAAGAGCAGAAATGATGGCAATCTTGTGCTCATGCGACCGACAGAT 479  
QY 180 ValLeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIle 199  
Db 480 GTGTCTCAACGGCTGTCCATCCCGCTCGGGCCAGCCCTGAAATCTACGAGCCACCATC 539  
QY 200 LysValLeuGlnGlnGlyHisPheGluAspAspAspProAspGlyPheLeuGly 217  
Db 540 AAGGTGCTTCAGCAGAGCCACTTTGAGAGTGAATGCCCGATGCTTTAAGC 593

RESULT 6  
B0671165  
LOCUS  
DEFINITION AGNCOURT 8032664 NIH\_MGC\_102 Homo sapiens cDNA clone IMAGE:6213736  
5', mRNA sequence.  
B0671165  
ACCESSION B0671165.1 GI:21781999  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 921)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LICM2379 row: c column: 17  
High quality sequence stop: 538.  
Location/Qualifiers  
1. 921  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6213736"

ORIGIN  
Alignment Scores:  
Pred. No.: 4,44e-55 Length: 921  
Score: 1030.00 Matches: 199  
Percent Similarity: 92.66% Conservative: 3  
Best Local Similarity: 91.28% Mismatches: 12  
Query Match: 88.03% Indels: 4  
DB: 13 Gaps: 1  
US-09-976-740-7 (1-217) x B0671165 (1-921)  
QY 1 GluGluArgValLeuGluGlySerGluGluGlnAspAspGluAspGluGln 20  
Db 145 GAAAGCCGAGTCTTGAAGAAAGAGAGAGAGATGAT-----CATGAAGTGAAGA 198  
QY 21 AspAspValSerGluGlySerGluValProGluSerAspArgProAlaGlyAlaGlnHis 40  
Db 199 GATGATGTGTCAAGAGGCTCTGAAGTGGCCGAGATGACCGCTTCGACGTTGCCAGAC 258  
QY 41 HisGlnLeuAsnGlyGluArgGlyProGlnSerAlaValGluArgValLeuGlyTrpThr 60  
Db 259 CACCAAGCTTAACGAGAGGAGGAGGAGCTCAGAGTCCAAAGAGAGGAGTCAAGAGTGGACC 318  
QY 61 ProCysGlyProHisIleGlnGlyGlnAspGluGlyArgGlyProAlaProGlySerGlyThr 80  
Db 319 CCGTGGAGCCGACACAGGAGGAGATGAAGGGCGGGGCCAGCCCGGGCAGCGGACC 378  
QY 81 ArgGlnValPheSerMetAlaAlaMetAsnGlyGlyGlyThrAlaSerValAlaThr 100  
Db 379 CGCCAGGTCTTCTCATGGCAGCCCATGAACAAAGAGAGGAGAAAGCTTGTGTCACACC 438  
QY 101 GlyProAspSerProSerProValProLeuProProGlyLysProAlaLeuProGlyAla 120  
Db 439 GGGCCAGATCTCCCGTCCCGCTGCTTGGCCCGCAGCAACAGCCCTACCTGGGGCC 498  
QY 121 AspGlyThrProPheGlyCysProProGlyArgGlyGlyLysProSerAspProValGlu 140  
Db 499 GACGGAGACCCCTTGGCTGTCTCCCGGGCCAAAGAGAACCATCTGATCCGTCAG 558  
QY 141 TrpThrValMetAspValValGluTrpPheThrGluValGlyPheProGluGlnAlaThr 160  
Db 559 TGGACCGTATGATGTCTGTCGAATATTCTAGAGCTGATTTCCCGAGAGGCGACA 618  
QY 161 AlaPheGlnGlnGlnIleAspGlyLysSerLeuLeuLeuMetGlnArgThrAspVal 180  
Db 619 GCTTCCCGCAGACAGAAATGATGAGCAAAATCTTGTGCTCATGACAGGGCGGATGTG 678  
QY 181 LeuThrGlyLeuSerIleArgLeuGlyProAlaLeuLysIleTyrGluHisIleLys 200  
Db 679 CTTCGGGGCTTTCATGCGCTCGGGCCACCTGAAATTTTACGATCACAGATCAG 738  
QY 201 ValLeuGln-GlnGlyHisPheGln-AspAspAspProAspGlyPheLeu 216  
Db 739 GGGCTTTCGACAGGGCCCTTTGAGAGGGTGAATGACCCGAGAGGCTTCTTA 788

RESULT 7  
BES13784  
LOCUS  
DEFINITION 601315608P1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3634417 5',  
mRNA sequence.  
ACCESSION BES13784

VERSION	BE513784.1	GI:9720996
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 686)	
TITLE	Nih-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	

Tissue Procurement: Louis M. Stauch, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at: [image.jlni.gov](http://image.jlni.gov)  
 Plate: L10M28 row: p column: 02  
 High quality sequence stop: 642.  
 Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="IMAGE:3634417"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NH MGc 8"
/notes="Organ: lymph. Vector: pORB7. Site 1: XhoI, Site 2:
EcoRI, cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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Alignment Scores:	
Pred. No.:	3,51e-55
Score:	1029.00
Percent Similarity:	96.76%
Best Local Similarity:	96.76%
Query Match:	87.95%
DB:	10
US-09-976-740-7 (1-217) x BE513784 (1-666)	
	Length: 686
	Matches: 209
	Conservative: 0
	Mismatches: 5
	Indels:
	Gaps: 0

[illegible]

QY	121	GI <sup>1</sup> ThrProPheGlyCysProProGlyValIleGlnIysProSerAspProValGlnTr	141
Db	402	CGGAGCCCCCTTTGGCTGTCTCCCGGGCGAAGAGAGCATGTATCCCGTGAAGTG	461
QY	141	PThrValMetAspValValGlnTrPheThrGlnIleAlaIlePheProGlnGlnIleAThrAl	161
Db	462	GACCGTAGTAGATGCTGCAGATATTTTACTGAGGCTGGATTTCCGGAGCGAGCGACACGC	521
QY	161	APheGlnIleGlnGlnIleAspGlyIleSerLeuIleuMetGlnArgTrnAspValIle	181
Db	522	TTTCCAAAGACAGAAATCGATGGCAATCTTTGTGTCTCATGACGCCACACAGATGTCT	581
QY	181	uThrGlyLeuSerIleArgLeuGlyProAlaLeuIleuIleTrpGlnIleShiIleIleVal	201
Db	582	CACGGGCTGTGCATCCGCCCTCGGGCGACGCTTGAAATC-TACGAGCC-CACATCAAGGT	639
QY	201	IleuGlnGlnGlnIleHisPheGlnIleAspAspProCaspGlyPheLeu	216
Db	640	GCTACGCCAGC--CACTTTAGGGGAGATTC--CCGATGCGCTTCTTA	682

RESULT 8	BE621115	590 bp	linear	EST 20-OCT-2000
LOCUS	6014993936p1	NIH_MGC_70	Homo sapiens	CDNA clone IMAGE:3896097 5',
DEFINITION	nrRNA sequence.			
ACCESSION	BE621115			
VERSION	BE621115.1	GI:3892053		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 590)			
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)			
	Unpublished (1999)			
	Contact: Robert Strausberg, Ph.D.			

FEATURES

CNA Library Preparation: Life Technologies, Inc.  
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMLN at:  
<http://image.llnl.gov>  
Plate: LRAM9688 row: 9 column: 10  
High quality sequence stop: 590.  
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3896097"
/tissue_type="epithelioid carcinoma"
/lab_host="RDH10B (phage-resistant)"
/clone_1db="NIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SpOst6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

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ORIGIN

Alignment Scores:

Pred. No.:	4.66e-55	Length:	590
Score:	1026.00	Matches:	189
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	87.69%	Indels:	0
DB:	10	Gaps:	0

US-09-976-740-7 (1-217) x BB621115 (1-590)

Db	1	GGCTCTGAAGTGGCCGAGAGTGAACCGTCTCTGAGGTGCCAGACCAACAGTTAACGGC	60
Qy	46	GIUARGIY-PROGINSERIALALYSGIUARGVALLYSGIUTPTPTPTProcygelyProhis	65
Db	61	GAGGGGGACCTCAGAGTGCACAGGAGGGGTCAAGAGGTGAGACCCCTGGGGACCGGAC	120
Qy	66	GINGIYGINAEPGJLYARGIYPRALAPROGYSERGIYTHARGIYNVALPHESER	85
Db	121	CAGGGCCAGAGTGAAGGGCGGGGGCCAGCCCGGGCAGCGGCACCCCAGGTGTTCTCC	180
Qy	86	METALAALMETASNLVSGIUGLYGLYTHRALASERVALATHRGILYPROASPSEPRO	105
Db	181	ATGGCAGCGCATGAACAGAGGGGGAGACAGCTTGTGTGGCACCGGGCCAGACTCCCGG	240
Qy	106	SERPROVALPROLEUPROPROGJLYIYSPHOLALEUPROGJLYALASGJLYTHPROPHE	125
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Qy	126	GLIYCSPPROPROGJLYARGIYSGIULIYSPROSEAPSPROVALGIUTPTPTVALMETASP	145
Db	301	GGCGTCTCTCCCGGGCGCAAGAGAGGCACTGTGATCCCGTGAAGTGACCGTATGAT	360
Qy	146	VALVALGIUTIYRPHETHGIULIAGIYPHEPROGIUNGINALATHRALPHEGINIUGLN	165
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Db	421	GAAATTGATGGCAATCTTTGTCTGTCAACGACGCAAGATGCTCAACGGGCTGTCC	480
Qy	186	ILEARGLEUGIYPROIALALEULYILETYGJUNISHIILEYSGVALLIUGINGIUGLY	205
Db	481	ATCGCGCTCGGGCCAGCCCTGAAATCTAACGAGCACCAATCAAGTGTCTTCAGCAAGC	540
Qy	206	HISPEGILUASPHASAPSPROASGJLY 214	
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**RESULT** 9  
**LOCUS** BM792162  
**DEFINITION** K-EST0072322 S22SNUL61 Homo sapiens cDNA clone S22SNUL61-15-C02  
5'', mRNA sequence.  
**ACCESSION** BM792162  
**VERSION** BM792162.1 GI:19140394  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eumetazoa; Euthera; Primates; Carnivora; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 568)  
**AUTHORS** Kim,N.S., Hamm,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.V., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
21c Frontier Korean EST Project 2001  
Unpublished (2002)  
**TITLE** Contact: Kim YS  
**JOURNAL** Genome Research Center  
**COMMENT** Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea  
Tel.: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
plate: 15 row: C column: 02  
High quality sequence stop: 568.

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location/Qualifiers
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Site: 2: Norti; The S22SNU16 library was contributed by the
Soares Laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al..
(1990), Cancer Res 50: 2773-2780. "

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Percent Similarity:	100.00%
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Query Match:	87.35%
Db:	12
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	Conservative: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

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QY	48	GLYProGlnSerAlaLysGluArgValLysGluTrpThrProCysGlgYProHisGlnGly	67
Db	63	GGACCTCAGAGTGCCTCAAGAGGGGTCAAGAGAGTGAACCCCTCGGACCCACAGAGGC	122
QY	68	GLInAspGlnGluYanArgYlProAlaLProGlySerLysThrArgGlnValPheSerMetAla	87
Db	123	CAGATGAGGGCCGGGGCCAGCCCCGGGACGGGACCCGCCAGAGTGTCTCCATGGCA	182
QY	88	AlaMetAsnLysGlnGlyGlyThrAlaSerValaLThrGlyProAspSerProSerPro	107
Db	183	GCCATGAACAAGAGAGGGGAGAACAGCTTCTGTTCACCCGGGGCAGACTCCCGGCCCCC	242
QY	108	ValLProLeuProProGlyLysProAlaLeuProGlyLysAlaAspGlyThrProPheGlyCys	127
Db	243	GTGGCTTTGCCCCCAGGCAACCAAGCCCTTACTGAGGCGCAGCGGACCCCTTTGGCTGT	302
QY	128	ProProGlyArgLysGluLysProSerAspProValGluTrpThrValMetAspValaL	147
Db	303	CCTCCCGGGCGCAAGAGAGACCATCTGATCCGTCGATGGACCGATGATGATGTGCTC	362
QY	148	GluTrpPheThrGlnAlaGlyPheProGluGlnAlaThrAlaPheGlnGluGlnLile	167
Db	363	GAATATTTTACTGAGGCTGTGATTTCCGAGACGAGCGACAGCTTTCCAAAGACAGAAATT	422
QY	168	AspGlyLysSerLeuLeuMetGlnArgThrAspValLeuThrGlyLeuSerLileArg	187
Db	423	GATGGCAATTTTGTCTGTCTATGACAGGACCAAGATGTCTCACGGCTCTCCATCCGC	482
QY	188	LeuGlyProAlaLeuLysLileTrpGluHisHisLileLysValLeuGlnGlnGlyHisPhe	207
Db	483	CTCGGGCCAGCGCCGGAAGATCTAAGAGACACATCAAGAGTTCACAGCAAGGCCACTTT	542
QY	208	GluAspAspAspProAspGlyPhe	215
Db	543	GAGGATGATGACCCCGATGCGCTTC	566
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LOCUS	602396526p1	NIH_MGC_94	Mus musculus CDNA clone IMAGE:451167 5',
DEFINITION	RNA sequence.		
BG298788			
ACCESSION	BG298788.1		
VERSION	GI:13063792		
1056 bp mRNA linear EST 21-FEB-2001			



QY 41 HisGlnLeuAnsngIyGluatArgIyProGlnSerAlaIySgluAryValIySgluTrrPThr 60  
 Db 224 CACCAAGCTTAACGGCGAGCGGGGAGCTCAGAGTCCCAAGAGAGGGGTCAAGAGGTGAGCC 283  
 QY 61 ProCGsGlyProHsngIyGlnIyAspGluGlyAryGlyProAlaProGlySerGlyThr 80  
 Db 284 CCTGCGGAGCCGACCA-GGCCAGATGAAGGGCGGGGCGACCCCGGGCAGCGGACC 342  
 QY 81 ArgGlnAlaPheSerMetAlaAlaMetAsnIySgluGlyGlyThrAlaSerValAlaThr 100  
 Db 343 CGCAGAGTGTCTTCATGAGCAGCATGACAGAGAAAGGGGAAACAGCTTCTGTGCGACC 402  
 QY 101 GLyProAspSerProSerProValProLeuProProGlyIySerProAlaLeuProGlyAla 120  
 Db 403 GGGCGAAGCTCCCGTCCCGGCTTTCGCGGCGCAAGCCAGCCCTGAGGAGCC 462  
 QY 121 AspGlyThrProPheGlyCySPProGlyAryIySgluIySProSerAspProValGlu 140  
 Db 463 GACGGAGACCCCTTGGCTGTCTCCCGGCGCAAGAGAGCATGTATCCCGTCGAG 522  
 QY 141 TyrThrValMetAspValIyGlu-TyrPheThrGluAla-GlyPhePro--GluGln 159  
 Db 523 TGGACCGTGAATGATGTCGTGAAATATTTACTGAGGCTTGATTTCCCGAGAGCAAG 582  
 QY 159 IaThrAlaPheGlnGluGlnIyLeuIyLeuAspIyIySerLeuLeuLeu-MetGln-ArgThr 178  
 Db 583 CGAGAGCTTTCAGAGAGAGAAATTAATGAGCAATCTTGTCTGCTCAATGAGCGGAC 642  
 QY 178 rAspValLeuThrGlyLeuSerIleAryLeuGlyProAlaLeuIyIyIyGlnIyHsH 198  
 Db 643 AGATGTGCTCACCGCTTGTTCATCCGCTCGGGCCAGC-CTGAAATCTACAGACCA 701  
 QY 198 sIleIyValLeuIyGlnIyGlnIyHsPheGluAsp-AspAspProAspGlyPheLeu 216  
 Db 702 CATCAAGGTGCTTACAGAG--CCACTTGAAGATTGATGACCCCGAGTGGTCTTA 754

RESULT 12  
 B1987692 600 bp mRNA linear EST 20-DEC-2001  
 LOCUS B1987692  
 DEFINITION 3204-64 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,  
 mRNA sequence.  
 ACCESSION B1987692  
 VERSION B1987692.1 GI:17958662  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 600)  
 Mu.X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W.,  
 White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.  
 Gene expression in the developing mouse retina by EST sequencing  
 and microarray analysis  
 Nucleic Acids Res. 29 (24), 4983-4993 (2001)  
 JOURNAL MEDLINE  
 MEDLINE 21671825  
 PUBMED 11812828  
 COMMENT Contact: Klein WH  
 Department of Biochemistry and Molecular Biology  
 University of Texas M.D. Anderson Cancer Center  
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA  
 Tel: 713 792 3646  
 Fax: 713 790 0329.  
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Alignment Scores:

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 Best Local Similarity: 92.82% Mismatches: 8  
 Query Match: 84.44% Indels: 0  
 DB: 12 Gaps: 0

US-09-976-740-7 (1-217) x B1987692 (1-600)

QY 23 ValSerGluIySerGluValProGluSerAspArgProAlaGlyAlaGlnHsGln 42  
 Db 3 GTATCTGAGGGCTCAGAAAGTGCCTGAGAGTACCCCGCAGGTGCTCAGACCATCAG 62  
 QY 43 LeuAsnGlyIyAryGlyProGlnSerAlaIySgluAryValIySgluTrrPThrProCs 62  
 Db 63 ATTAAAGAGAGCGGGCCCTAGAGTGTAAAGAGAGGTCAAGAGTGTGCTGCT 122  
 QY 63 GLyProHsngIyGlnIyAspGluGlyAryGlyProAlaProGlyIySerGlyThrArgGln 82  
 Db 123 GGAACCTACAGAGGCGAGATGAAGGGGAGCACGACCTGCGACAGCGAG 182  
 QY 83 ValPheSerMetAlaAlaMetAsnIySgluGlyGlyThrAlaSerValAlaThrGlyPro 102  
 Db 183 GTGTTCCTCCATGACAGCTGTGATTAAGAGGGGATATCAGCTTGTGTGAGACAGCTCA 242  
 QY 103 AspSerProSerProValProLeuProProGlyIySProAlaLeuProGlyAlaAspGly 122  
 Db 243 GATTCCTCATCTCCGGTGTGCTTGTCTCCAGAAACAGCCCTACCTGGGGCTGATGG 302  
 QY 123 ThrProPheGlyCySPProGlyAryIySgluIySProSerAspProValGluTrrPThr 142  
 Db 303 AACCTTTTGGCTGTCTCCCGGCGCAAGGAGGAGCCGACAGCCAGTGAAGGAGCA 362  
 QY 143 ValMetAspValIyGluIyPheThrGluIyIyPheProGluGlnAlaThrAlaPhe 162  
 Db 363 GTCATGATGATGTGGATATCTTCACTGAGCGGGCTTCCAGACAGCGCCCTCTTT 422  
 QY 163 GlnGluGlnIyIyAspGlyIySProAlaLeuLeuMetGlnArgThrAspValLeuThr 182  
 Db 423 CAGAGCAGAGAAATGATGAGCAAGTCTTGTGCTCATGCAACGAGATGCTGCTACT 482  
 QY 183 GlyLeuSerIleAryLeuGlyProAlaLeuIyIyIyGlnIyHsHsIleIyValLeu 202  
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 VERSION BE270987.1 GI:9144634  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 829)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: InCyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at: image.llnl.gov









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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:49:56 ; Search time 227.827 Seconds  
(without alignments)

2853.675 Million cell updates/sec

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Perfect score: 82  
Sequence: 1 EEEEDDEDEDEDD 15Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-CUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	82	100.0	45 6 AR374690	AR374690 Sequence
3	82	100.0	45 6 AR409325	AR409325 Sequence
4	82	100.0	45 6 AX239587	AX239587 Sequence
5	82	100.0	45 6 BD056452	BD056452 Novel low
6	82	100.0	78 6 AR199539	AR199539 Sequence
7	82	100.0	78 6 AR374691	AR374691 Sequence
8	82	100.0	78 6 AR409326	AR409326 Sequence
9	82	100.0	78 6 AX239588	AX239588 Sequence
10	82	100.0	78 6 BD056453	BD056453 Novel low
11	82	100.0	982 6 BC007384	BC007384 Homo sapi
12	82	100.0	1208 6 AR199535	AR199535 Sequence
13	82	100.0	1208 6 AR374687	AR374687 Sequence
14	82	100.0	1208 6 AR409322	AR409322 Sequence
15	82	100.0	1208 6 AX239573	AX239573 Sequence
16	82	100.0	1208 6 BD056449	BD056449 Novel low
17	82	100.0	1470 6 BC030129	BC030129 Homo sapi
18	82	100.0	1614 6 AR409337	AR409337 Sequence
19	82	100.0	1614 6 AX239602	AX239602 Sequence
20	82	100.0	1617 9 AY453840	AY453840 Homo sapi
21	82	100.0	12425 6 AR409341	AR409341 Sequence
22	82	100.0	12425 6 AX239607	AX239607 Sequence
23	82	100.0	12425 6 AC022098	AC022098 Homo sapi
24	79	96.3	1521 4 OAU35655	U35655 Ovis aries
25	76	92.7	335 5 PFU538319	PFU538319 plactich
26	76	92.7	29150 8 AC115683	AC115683 Dictyost
27	75	91.5	1442 8 SOTSNAIP	L38856 Glycine max
28	75	91.5	152564 10 AC127549	AC127549 Mus muscu
29	75	91.5	177408 2 AC115847	AC115847 Mus muscu
30	75	91.5	233181 2 AC111558	AC111558 Rattus no
31	74	90.2	1249 10 BC019416	BC019416 Mus muscu
32	74	90.2	2576 5 GGNWCC23	X17199 Chicken mRN
33	74	90.2	3452 5 D88440	D88440 Gallus gall
34	74	90.2	12028 3 AE001412	AE001412 Plasmodiu
35	74	90.2	68671 2 AC101600	AC101600 Mus muscu
36	74	90.2	110000 2 BX571702	Continuation (3 of
37	74	90.2	169094 10 AC129013	AC129013 Mus muscu
38	74	90.2	172611 2 AC121664	AC121664 Rattus no
39	74	90.2	197650 2 AC107704	AC107704 Mus muscu
40	74	90.2	204911 10 AC1099169	AC1099169 Mus muscu
41	74	90.2	213739 2 AC113937	AC113937 Mus muscu
42	74	90.2	217932 2 AC115817	AC115817 Mus muscu
43	74	90.2	220554 2 AC112111	AC112111 Rattus no
44	74	90.2	223318 10 BX284111	BX284111 Mouse DNA
45	74	90.2	239824 2 AC121166	AC121166 Rattus no

## ALIGNMENTS

RESULT 1

AR199538 45 bp DNA linear PAT 20-APR-2002  
LOCUS AR199538  
DEFINITION Sequence 30 from patent US 6355451.  
ACCESSION AR199538  
VERSION AR199538.1 GI:20249612  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 30 12-MAR-2002;  
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DEFINITION Sequence 30 from patent US 6605588.  
ACCESSION AR374690  
VERSION AR374690.1 GI:40077505  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 30 12-AUG-2003;  
FEATURES  
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DEFINITION Sequence 30 from patent US 6632923.

ACCESSION AR409325 GI:40160113  
VERSION AR409325.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 45)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 30 14-OCT-2003;  
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Db 1 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 4  
LOCUS AX239587 45 bp DNA linear PAT 26-SEP-2001  
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ACCESSION AX239587  
VERSION AX239587.1 GI:15797263  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
JOURNAL Low density lipoprotein binding proteins and their use in diagnosing  
Patent: WO 0164874-A 30 07-SEP-2001;  
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Pred. No.: 0.000235 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-19 (1-15) x AX239587 (1-45)

Qy 1 GUGUGUGUGUUAASPAPSPGUAAPGUAAPGUGUUAASPASP 15  
Db 1 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 5  
LOCUS BD056452 45 bp DNA linear PAT 27-AUG-2002  
DEFINITION Novel low density lipoprotein binding proteins and their use in

diagnosing and treating atherosclerosis.

ACCESSION BD056452  
 VERSION GI:22602058  
 KEYWORDS JP 2001506983-A/10.  
 SOURCE Aequorea victoria  
 ORGANISM Aequorea victoria  
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Leptomedusae; Aequoreidae; Aequorea.

REFERENCE 1 (bases 1 to 45)  
 AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
 TITLE Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis  
 JOURNAL Patent: JP 2001506983-A 10 29-MAY-2001;  
 BOSTON HEART FOUNDATION INC  
 COMMENT PN JP 2001506983-A/10  
 PD 29-MAY-2001  
 PF 26-NOV-1997 JP 1998524870  
 PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI  
 ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
 A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K51/08, PC  
 C07H21/00,  
 PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC  
 Strandedness: Single;  
 Topology: Linear;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers

FEATURES  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.000235 Length: 45  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-19 (1-15) x BD056452 (1-45)

QY 1 G|U|G|U|G|U|G|U|A|S|P|A|S|P|A|S|P|G|U|A|S|P|G|U|G|U|A|S|P|A|S|P 15  
 Db 1 GAAAGAGAAAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 6  
 ARI99539  
 LOCUS ARI99539 78 bp DNA linear PAT 20-APR-2002  
 DEFINITION Sequence 31 from patent US 6355451.  
 ACCESSION ARI99539  
 VERSION ARI99539.1 GI:20249613  
 KEYWORDS  
 ORGANISM Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 78)  
 AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
 TITLE Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis  
 JOURNAL Patent: US 6355451-A 31 12-MAR-2002;  
 FEATURES Location/Qualifiers  
 source 1..78  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.000399 Length: 78  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

DB: 6 Gaps: 0

US-09-976-740-19 (1-15) x ARI99539 (1-78)

QY 1 G|U|G|U|G|U|G|U|A|S|P|A|S|P|G|U|A|S|P|G|U|G|U|A|S|P|A|S|P 15  
 Db 1 GAAAGAGAAAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 7  
 AR374691  
 LOCUS AR374691 78 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 31 from patent US 6605588.  
 ACCESSION AR374691  
 VERSION AR374691.1 GI:40077506  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 78)  
 AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
 TITLE Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis  
 JOURNAL Patent: US 6605588-A 31 12-AUG-2003;  
 FEATURES Location/Qualifiers  
 source 1..78  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.000399 Length: 78  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-19 (1-15) x AR374691 (1-78)

QY 1 G|U|G|U|G|U|G|U|A|S|P|A|S|P|G|U|A|S|P|G|U|G|U|A|S|P|A|S|P 15  
 Db 1 GAAAGAGAAAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 8  
 AR409326  
 LOCUS AR409326 78 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 31 from patent US 6632923.  
 ACCESSION AR409326  
 VERSION AR409326.1 GI:40160114  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 78)  
 AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
 TITLE Low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis  
 JOURNAL Patent: US 6632923-A 31 14-OCT-2003;  
 FEATURES Location/Qualifiers  
 source 1..78  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 0.000399 Length: 78  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-19 (1-15) x AR409326 (1-78)

QY 1 G1UG1UG1UG1UASPASPGLUASPGLUASPGLUASPASP 15  
 DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 9  
 LOCUS AX239588 78 bp DNA linear PAT 26-SEP-2001  
 DEFINITION Sequence 31 from Patent WO0164874.  
 ACCESSION AX239588  
 VERSION AX239588.1 GI:15797264  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Low density lipoprotein binding proteins and their use in diagnosing  
 and treating atherosclerosis  
 Patent: WO 0164874-A 31 07-SEP-2001;  
 Boston Heart Foundation, Inc. (US)

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Alignment Scores:  
 Pred. No.: 0.000399 Length: 78  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-19 (1-15) x AX239588 (1-78)

QY 1 G1UG1UG1UG1UASPASPGLUASPGLUASPGLUASPASP 15  
 DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 10  
 LOCUS BD056453 78 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Novel low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis.  
 ACCESSION BD056453  
 VERSION BD056453.1 GI:22602059  
 KEYWORDS JP 2001506983-A/11.  
 SOURCE Aequorea victoria  
 ORGANISM Aequorea victoria  
 Eukaryota; Metazoa; Chordata; Hydrozoa; Hydrozoa; Leptomedusae;  
 Aequorea; Aequorea.  
 1 (bases 1 to 78)

REFERENCE 1  
 Lees, A.M., Lees, R.S., Law, S.W. and Arjona, A.A.  
 Novel low density lipoprotein binding proteins and their use in  
 diagnosing and treating atherosclerosis  
 Patent: JP 2001506983-A 11 29-MAY-2001;  
 BOSTON HEART FOUNDATION INC  
 PN JP 2001506983-A/11  
 PD 29-MAY-2001  
 PR 26-NOV-1997 JP 1998524870  
 PR 27-NOV-1996 US 60/031930, 03-JUN-1997 US 60/048547 PI  
 ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC  
 A61K38/04, A61K38/17, A61K39/00, A61K48/00, A61K49/00, A61K51/08, PC  
 C07H21/00,  
 PC C07K7/00, C07K14/705, C12N15/12, C12Q1/02, C12Q1/68, G01N33/566 CC  
 Strandness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
 Location/Qualifiers

source 1..78  
 /organism="Aequorea victoria"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:6100"

ORIGIN

Alignment Scores:  
 Pred. No.: 0.000399 Length: 78  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: Gaps: 0

US-09-976-740-19 (1-15) x BD056453 (1-78)

QY 1 G1UG1UG1UG1UASPASPGLUASPGLUASPGLUASPASP 15  
 DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 11  
 LOCUS BC007384 982 bp mRNA linear PRI 16-SEP-2003  
 DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone  
 IMAGE:3877194), partial cds.  
 ACCESSION BC007384  
 VERSION BC007384.2 GI:33988219  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 (bases 1 to 982)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heib, F.,  
 Dietzenko, L., Marsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Scheetz, T.E., Brownstein, M.U., Ushin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.U.,  
 Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.U.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalske, U., Smailus, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257  
 PUBMED 12477932

REFERENCE 2 (bases 1 to 982)  
 Strausberg, R.  
 Direct Submission  
 Submitted (01-MAY-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK  
 NTH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 On Aug 20, 2003 this sequence version replaced gi:13938477.  
 Contact: MGC help desk  
 Email: [cgaps-rcmail.nih.gov](mailto:cgaps-rcmail.nih.gov)  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnln.gov>  
Series: IRAL Plate: 24 Row: 9 Column: 10.  
Location/Qualifiers

## FEATURES

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/clone\_id="NIH MGC-8"  
/lab\_host="DH10B-R"  
/note="Vector: pOT87"  
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/note="SAM; Region: Sterile alpha motif. Widespread domain  
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proteins to a conserved tyrosine that is phosphorylated.  
In many cases mediates homodimerisation"  
/db\_xref="CDD:smart00454"

## CDS

gene

misc\_feature

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00456 Length: 982  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-19 (1-15) x BC007384 (1-982)

QY 1 GIUGIUGIUGIUAASPAPSPGIUASPGLIUGIUAASP 15

Db 79 GAAGAGAGAGAGATGATGATGAGATGAGATGAGAGATGAT 123

## RESULT 12

LOCUS AR199535 1208 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 16 from patent US 6355451.  
ACCESSION AR199535  
VERSION AR199535.1 GI:20249609  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1208)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 16 12-MAR-2002;  
FEATURES Location/Qualifiers  
1..1208

JOURNAL  
FEATURES  
SOURCE 1..1208

/organism="unknown"  
/mol\_type="unassigned DNA"

Alignment Scores:  
Pred. No.: 0.00557 Length: 1208  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-19 (1-15) x AR199535 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPSPGIUASPGLIUGIUAASP 15

Db 22 GAAGAGAGAGATGATGATGAGATGAGATGAGAGATGAT 66

## RESULT 13

LOCUS AR374687 1208 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 16 from patent US 6605588.  
ACCESSION AR374687  
VERSION AR374687.1 GI:40077502  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1208)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 16 12-AUG-2003;  
FEATURES Location/Qualifiers  
1..1208  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00557 Length: 1208  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-09-976-740-19 (1-15) x AR374687 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPSPGIUASPGLIUGIUAASP 15

Db 22 GAAGAGAGAGATGATGATGAGATGAGATGAGAGATGAT 66

## RESULT 14

LOCUS AR409322 1208 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 16 from patent US 6632923.  
ACCESSION AR409322  
VERSION AR409322.1 GI:40160110  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1208)  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 16 14-OCT-2003;  
FEATURES Location/Qualifiers  
1..1208  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:48:14 ; Search time 23.776 Seconds

(without alignments)  
2680.137 Million cell updates/sec

Title: US-09-976-740-19

Perfect score: 82

Sequence: 1 EEEEDDEDEDEED 15

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	82	100.0	1336	3	AAH21860
6	82	100.0	1614	5	AAH26499
7	82	100.0	12425	5	AAH26495
8	74	90.2	2919	3	AAA70216

9	73	89.0	2044	3	AAZ43754	AAZ43754 Murine NN
10	73	89.0	4599	2	AAZ27052	AAZ27052 RRP3 telo
11	72	87.8	643	3	AAZ44095	AAZ44095 Arabidops
12	72	87.8	872	6	AAH98791	AAH98791 Arabidops
13	72	87.8	893	3	AAZ42206	AAZ42206 Arabidops
14	72	87.8	1284	6	AAZ32099	AAZ32099 Candida a
15	72	87.8	15790	6	ABQ76615	ABQ76615 C. albica
16	72	87.8	2442	6	ABQ76613	ABQ76613 C. albica
17	72	87.8	454	6	ABE63824	ABE63824 Breast ca
18	71	86.6	454	6	ABH95865	ABH95865 Gene #246
19	71	86.6	833	3	AAH39731	AAH39731 Gastric c
20	71	86.6	1007	2	AAH39730	AAH39730 Gastric c
21	71	86.6	1962	7	ABQ77438	ABQ77438 Human CGD
22	71	86.6	2142	6	ABK63660	ABK63660 Rat seqe
23	71	86.6	2142	7	ABH41831	ABH41831 Toxicity-
24	71	86.6	2142	9	ADB58108	ADB58108 Toxicity-
25	71	86.6	2142	9	ADB52591	ADB52591 Primary r
26	71	86.6	2463	9	ADB89111	ADB89111 Encoding
27	71	86.6	2495	4	ABH14237	ABH14237 Drosophil
28	71	86.6	2736	6	ABK84322	ABK84322 Human CDN
29	71	86.6	2736	9	ADB31350	ADB31350 Bicalutam
30	71	86.6	2824	7	ABQ77434	ABQ77434 Human CGD
31	71	86.6	2806	7	ABQ77440	ABQ77440 Human CGD
32	71	86.6	3005	7	ABQ77439	ABQ77439 Human CGD
33	71	86.6	4167	4	ABH12108	ABH12108 Drosophil
34	71	86.6	5402	4	ABH14236	ABH14236 Drosophil
35	71	86.6	7585	2	AAV68403	AAV68403 Human BAZ
36	71	86.6	7585	2	ACR34516	ACR34516 Gene enco
37	70	85.4	190	3	AAH07764	AAH07764 Human sec
38	70	85.4	402	2	AAH20520	AAH20520 Human gen
39	70	85.4	430	2	ADD49446	ADD49446 Human lun
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43	70	85.4	576	5	AAH84117	AAH84117 DNA enco
44	70	85.4	592	5	ABH44417	ABH44417 Human pro
45	70	85.4	703	6	ABH77067	ABH77067 Frog embr

## ALIGNMENTS

RESULT 1	AAH26502	standard; DNA; 45 BP.
XX	AAH26502	
AC	AAH26502	
XX	AAH26502	
DT	12-NOV-2001	(first entry)
XX	12-NOV-2001	
DE	Low density lipoprotein binding protein (LBP) polynucleotide.	
XX	Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis;	
KW	antiartherosclerotic; therapy; diagnosis; vaccine; ss.	
KM		
XX		
OS	Mammalia.	
XX		
EN	WO200164874-A2.	
PD	07-SEP-2001.	
XX		
PF	28-FEB-2001; 2001WO-US006356.	
XX		
PR	02-MAR-2000; 2000US-00517849.	
PR	14-JUL-2000; 2000US-00616289.	
XX		
PA	(BOST-) BOSTON HEART FOUND INC.	
XX		
PI	Lees AM, Lees RS, Law SW, Arjona AA;	
XX	WPI; 2001-565505/63.	
DR		
XX		
PT	New isolated low density lipoprotein binding polypeptide for treating,	
PT	diagnosing and/or identifying therapeutic agents for atherosclerosis.	

CC The present sequence is that of polynucleotide encoding a fragment of  
CC novel low density lipoprotein binding proteins (LDLPs) of the invention  
CC (see AA82797-82) LDLPs are capable of binding to native and methylated  
CC (see AA82797-82) LDLPs are capable of binding to native and methylated  
CC low density lipoproteins (LDLPs). Isolated polynucleotides encoding novel  
CC LDLPs and their fragments are claimed, as well as expression vectors,  
CC cells and methods of producing the LDLPs. Methods of determining if an  
CC animal is at risk for atherosclerosis, methods for evaluating an agent

PT Nucleic acid encoding low density lipoprotein binding proteins and related vectors - transformed cells, proteins, and modulators of binding,

PT useful for treatment and diagnosis of atherosclerosis and for identifying  
PT subjects at risk.  
XX



XX PS Claim 1; Page 670-671; 1299pp; English.

XX CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human

CC CC proteins AAB58711 - AAB59128. The DNA and protein sequences are

CC associated with breast and ovarian cancer. Included in the invention are

CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the

CC isolation and characterization of the DNA and protein sequences of the

CC invention. The breast and ovarian cancer associated DNA, protein, agonist

CC or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic;

CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;

CC antiinflammatory; antitumor; vulnery; anticonvulsant; antibacterial;

CC antifungal; antiparasitic and cardiant activity. The polynucleotide and

CC protein sequences are used in the diagnosis of cancer, particularly

CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists

CC and agonists may also be used in the diagnosis, prevention and treatment

CC of immune disorders e.g. Addison's disease, allergies, autoimmune

CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;

CC cardiovascular disorders such as myocardial ischaemia; wound healing;

CC neurological diseases such as cerebral anoxia and epilepsy; and

CC infectious diseases

XX SQ Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;

XX Alignment Scores:

Pred. No.:	0.00938	Length:	1336
Score:	82.00	Matches:	15
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-976-740-19 (1-15) x AAF21860 (1-1336)

QY 1 GlUGlUGlUGlUAspAspAspGluAspGluAspGluAspAsp 15

DB 94 GAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 138

RESULT 6

AAH26499

ID AAH26499 standard; DNA; 1614 BP.

XX AC AAH26499;

XX DT 12-NOV-2001 (first entry)

XX DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.

XX KM Low density lipoprotein binding protein 2; LBP-2; LDL; human;

XX KM atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

XX KM ds.

XX OS Homo sapiens.

XX PN WO200164874-A2.

XX PD 07-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006356.

XX PR 02-MAR-2000; 2000US-00517849.

XX PR 14-JUL-2000; 2000US-00616289.

XX PA (BOST-) BOSTON HEART FOUND INC.

XX PI Lees AM, Lees RS, Law SM, Arjona AA;

XX DR WPI, 2001-565505/63.

XX DR P-PSDB; AAB82806.

XX PT New isolated low density lipoprotein binding polypeptide for treating,

PT diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX PS Claim 7; Fig 7A; 143pp; English.

XX CC The present sequence is that of the coding region of the human gene (see

CC also AAH26499) encoding novel human low density lipoprotein binding

CC protein 2 (LBP-2; see AAB82806). The gene was isolated from a genomic DNA

CC library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the

CC present sequence differs from that predicted from a cDNA clone (see

CC AAH28803) in that it contains an additional 321 amino acids at its N-

CC terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among

CC claimed polynucleotides of the invention that encode novel polypeptides

CC capable of binding to native and methylated LDL. Also claimed are

CC isolated LBP polypeptides, and biologically active fragments and

CC analogues of them, as well as expression vectors, cells and methods of

CC producing the LBPs. Methods of determining if an animal is at risk for

CC atherosclerosis, methods for evaluating an agent for use in treating

CC atherosclerosis, and methods for treating a cell having an abnormality in

CC structure or metabolism of LBP are claimed. Pharmaceutical compositions

CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions,

CC are also claimed

XX SQ Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	0.0112	Length:	1614
Score:	82.00	Matches:	15
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-976-740-19 (1-15) x AAH26499 (1-1614)

QY 1 GlUGlUGlUGlUAspAspAspGluAspGluAspGluAspAsp 15

DB 985 GAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 1029

RESULT 7

AAH26495

ID AAH26495 standard; DNA; 12425 BP.

XX AC AAH26495;

XX DT 12-NOV-2001 (first entry)

XX DE Human low density lipoprotein binding protein 2 (LBP-2) gene.

XX KM Low density lipoprotein binding protein 2; LBP-2; LDL; human;

XX KM atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;

XX KM ds.

XX OS Homo sapiens.

XX FH Key

XX FH CDS

XX FT Location/Qualifiers

XX FT 2832..5153

XX FT /\*tag= a

XX FT /note= "includes introns"

XX FT 2832..3785

XX FT /\*tag= b

XX FT 3786..4207

XX FT /\*tag= c

XX FT exon

XX FT 4208..4502

XX FT /\*tag= d

XX FT intron

XX FT 4503..4593

XX FT /\*tag= e

XX FT exon

XX FT 4594..4694

XX FT /\*tag= f

XX FT intron

XX FT 4695..4787

XX FT /\*tag= g

XX FT exon

XX FT 4788..4899

XX FT /\*tag= h

XX FT intron

XX FT 4900..4994

XX FT /\*tag= i



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FH   Key               location/Qualifiers
FT   CDS                77..1450
                               /*tag=a
                               /product= "NNX3"
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PN   MO9960115-A2.
PD   25-NOV-1999.
PE   17-MAY-1999;    99MO-EP003374.
PR   18-MAY-1998;    98EP-00201642.
PA   (VLAAM-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Van Leuven F;
XX
DR   WPI, 2000-053295/04.
DR   P-PSDB; AAY50875.
PT
PT   Novel proteins useful as markers and for treating lung tumors and/or
XX   Hodgkin's disease.
PS
PS   Claim 5; Page 45-47; 50pp; English.
XX
CC   This invention describes two novel NNX3 proteins isolated from human and
CC   murine sources which have cytostatic activity. The NNX3 mRNA and/or
CC   cDNA are useful as a marker for lung tumors or Hodgkin's disease. The
CC   proteins form pharmaceutical compositions useful for treating lung tumor
CC   and/or Hodgkin's disease. Polynucleotide products of the invention form
CC   an assay for screening the expression of these nucleic acids. Antibodies
CC   raised against the proteins of the invention form an assay for detecting
CC   the proteins. The probes form an assay for detecting and/or amplifying
CC   NNX3 polynucleotides. The expression of NNX3 in humans and mice suggest
CC   that NNX3 is useful as a marker for lung tumors and Hodgkin's disease.
CC   Therefore, the protein facilitates therapies for these conditions. This
CC   sequence encodes the murine NNX3 protein described in the method of the
CC   invention
XX
SQ   Sequence 2044 BP; 630 A; 400 C; 482 G; 532 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.:          0.234           Length:          2044
Score:              73.00         Matches:           12
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Best Local Similarity: 80.00%      Mismatches:       0
Query Match:        89.02%         Indels:           0
DB:                  3             Gaps:              0
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OY   1 GlUGlUGlUGlUAsPAsPaSgGUAsPgGUAsPgGlUGlUAsPaSP 15
Db   761 GAAGAAAGAGAAGATGCATGCATGCATGCATGCATGAAGAAGATGACGAT 805
RESULT 10
AAT27052 ID AAT27052 standard; DNA, 4599 BP.
XX AAT27052;
XX 12-OCT-1996 (first entry)
XX DE RRP3 telomerase-associated protein gene.
XX
XX Yeast; RRP3 gene; telomerase-associated protein; STR7;
KM suppressor of telomeric repression-7; telomerase; ribonucleoprotein;
KM telomere; tumour; pathogen; sperm; ovum; reporter gene; drug screening;
KM antibody; immunoassay; antitumour; antiseptic; contraceptive;
XX infertility; diagnostic; gene therapy; ss.
XX Saccharomyces cerevisiae.
XX
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FH Key Location/Qualifiers
FT CDS 835..4092
FT //tag= a
FT /product= "RRP3 protein"
FT
PV W09612811-A2.
PD 02-MAY-1996.
PP 20-OCT-1995; 95WO-US013801.
PR 20-OCT-1994; 94US-00326781.
PR 28-APR-1995; 95US-00431080.
PA (ARCH-) ARCH DEV CORP.
PI Gottschling DE, Singer MS;
XX WPI; 1996-239169/24.
DR P-PSTD; AAR95607.
XX
PT Novel telomerase associated polypeptide(s) and related nucleic acid -
PT useful for detecting e.g. tumour cells or pathogens.
XX
XX Example 10; Page 287-293; 349pp; English.
XX
XX The RRP3 gene encodes a telomerase-associated protein (with a fragment,
CC STR7, shown in AAT27051) found in conjunction with Saccharomyces
CC cerevisiae telomerase, a ribonucleoprotein required for telomere
CC replication. Other genes associated with telomerase are given in AAT27044
CC (telomerase RNA template gene) and AAT27046-50 (other STR genes). These
CC genes combine with telomerase to repress telomere silencing or gene
CC expression. Oligonucleotides from the sequence may be used to detect non-
CC ciliate telomerase-associated genes, e.g. in tumour, pathogen, sperm or
CC ovum cells. New telomerase-associated sequences may be detected by a
CC reporter gene expression system linked to an expression-repressing
CC telomere sequence, and binding compounds, e.g. antibodies, may be
CC detected by complex formation with telomerase components. The products
CC may be used as antitumour, anti-septic or contraceptive agents, in
CC infertility diagnosis, or in gene therapy
XX
SQ Sequence 4599 BP; 1717 A; 779 C; 898 G; 1205 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0.506 Length: 4599
Score: 73.00 Matches: 12
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 80.00% Mismatches: 0
Query Match: 89.02% Indels: 0
Gaps: 0
DB: 2
US-09-976-740-19 (1-15) x AAT27052 (1-4599)
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Db 1231 GAAGAAAGAAGATGATGCACGAAGCGACGACGATGATGAT 1275
|||||
RESULT 11
AAC44095 ID AAC44095 standard; DNA; 643 BP.
XX AAC44095;
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41614.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX

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us-09-976-740-19.rng

Page 7

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XX      06-SEP-2000.
XX      25-FEB-2000; 2000EP-00301439.
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Cy 1 GUGUGUGUGUUAAPAPAPAPAGUASPGLUASPGLUASPGLUASPAP 15  
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ID AAC42206 standard; DNA; 893 BP.  
XX AC AAC42206;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34680.  
XX KM Hybridisation assay; genetic mapping; gene expression control;  
XX KM protein identification; signal transduction pathway; metabolic pathway;  
XX KM promoter; termination sequence; ss.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
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PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
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PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
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PR 19-JUL-1999; 99US-0144335P.  
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PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
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PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
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 PR 23-AUG-1999; 99US-0149930P.  
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 PR 30-AUG-1999; 99US-0151303P.  
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 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157117P.  
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 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
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 PR 13-OCT-1999; 99US-0159295P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
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 PR 22-OCT-1999; 99US-0160980P.  
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 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
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PR 29-OCT-1999; 99US-0162142P.  
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 Score: 72.00 Matches: 12  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 87.80% Indels: 0  
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 Db 596 GAGAGGAGAGGATGCGATGATGATGACGACGAGAGAGAC 640  
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 ID AB232099 standard; DNA; 1284 BP.  
 AC AB232099;  
 XX 30-JAN-2003 (first entry)  
 DT  
 XX  
 DE Candida albicans essential gene SEQ ID NO 6386.  
 KM Fungus; yeast; tetracycline promoter; GRACE strain; biosynthesis;  
 KM signal transduction; DNA replication; cell division; growth; ss.  
 KM proliferation; Candida albicans; fungicide; antifungal; gene; ss.  
 XX  
 OS Candida albicans.  
 XX  
 PN WO200253728-A2.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 26-DEC-2001; 2001WO-US049486.  
 XX  
 PR 29-DEC-2000; 2000US-0259128P.  
 PR 20-FEB-2001; 2001US-0079202A.  
 PR 22-AUG-2001; 2001US-0314050P.  
 XX  
 PA (EDIT-) ELITRA PHARM INC.  
 XX  
 PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;  
 XX WPI; 2002-566694/60.  
 DR P-FSDB; ABP73549.  
 DR  
 XX  
 XX Constructing strains for identifying gene products as effective targets  
 PT for therapeutic intervention, by inactivating in the strain one allele of  
 PT a gene and placing other allele of the gene under conditional expression.  
 PT  
 XX  
 PS Claim 37; SEQ ID NO 6386; 167bp + Sequence Listing; English.  
 XX  
 CC The invention relates to constructing (M1) a strain of diploid fungal  
 CC cells in which both alleles of a gene are modified, comprising modifying  
 CC one allele by insertion or replacement by a cassette having an  
 CC expressible selectable marker and modifying other allele by  
 CC recombination, of a promoter replacement fragment with a heterologous  
 CC promoter, (M1) is useful for constructing a strain of diploid fungal  
 CC cells in which both alleles of a gene are modified. The diploid fungal  
 CC cells having both alleles modified are useful for identifying a gene that  
 CC is essential to the survival or growth of a fungus, a gene that  
 CC contributes to the virulence and/or pathogenicity of a fungus, a gene  
 CC that contributes to the resistance and/or pathogenicity of a fungus, a  
 CC agent, an antifungal agent that inhibits the growth of a mammalian  
 CC and for identifying a therapeutic agent for treatment of a mammalian  
 CC disease. (M1) is useful for identifying a compound which modulates the  
 CC activity of a gene product, preferably enzymatic activity, carbon  
 CC compound catabolism, biosynthetic, transporter, transcriptional,  
 CC translational, signal transduction, DNA replication and cell division

CC activity. The method is useful for identifying a compound having the  
 CC ability to inhibit growth or proliferation of *C. albicans* cells and for  
 CC treating infection by *C. albicans*. The present sequence is that of an  
 CC essential *Candida albicans* gene used in the method of the invention.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification but is based on sequence information supplied to Derwent by  
 CC the European Patent Office

XX SQ Sequence 1284 BP; 581 A; 156 C; 255 G; 292 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 0.205 Length: 1284  
 Score: 72.00 Matches: 12  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 87.80% Indels: 0  
 DB: 6 Gaps: 0

US-09-976-740-19 (1-15) x ABZ32099 (1-1284)

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 DB 400 GAGGAGGAGAGATGATGACGACGACGATGAAGAGGATGAC 444

RESULT 15  
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 ID ABQ76615 standard; CDNA; 15790 BP.  
 XX AC ABQ76615;  
 XX DT 21-NOV-2002 (first entry)  
 XX DE C. albicans BAX-associated CDNA fragment SEQ ID 655.  
 XX KW Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;  
 XX KM vasotropic; vaccine; gene therapy; proliferative disorder; cancer;  
 XX KM apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;  
 XX KM neurodegeneration; cell death; ss.  
 XX OS Candida albicans.  
 XX PN WO200264766-A2.  
 XX PD 22-AUG-2002.  
 XX PF 21-DEC-2001; 2001WO-EP015398.  
 XX PR 22-DEC-2000; 2000EP-00870318.  
 XX PR 04-JAN-2001; 2001EP-00870002.  
 XX PR 09-JAN-2001; 2001EP-00870003.  
 XX PA (JANC) JANSSEN PHARM NV.  
 XX PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;  
 XX DR WPI; 2002-667002/71.  
 XX DR P-PDB; ABG3349.  
 XX PT New isolated nucleic acid representing a synthetic BAX-gene, useful as  
 PT medicament for treating, preventing and/or alleviating yeast or fungal  
 PT infections or proliferative disorders, or for preventing apoptosis in  
 PT certain diseases.  
 XX PS Claim 36; Fig 2; 344pp; English.  
 XX CC This invention describes a novel nucleic acid representing a synthetic  
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-  
 CC resistant yeast or fungi, identifying, or obtaining and identifying  
 CC Candida spp. sequences that are differentially expressed in a pathway  
 CC eventually leading to programmed cell death or identifying inhibitors or  
 CC inhibitor sequences of Bax-induced cell death. The products of the  
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and  
 CC vasotropic activity and can be used in vaccines or for gene therapy. The

CC isolated nucleic acids, polypeptides, pharmaceutical compositions,  
 CC antisense molecules and antibodies are useful as medicaments or in  
 CC preparing a medicament for treating, preventing and/or alleviating  
 CC diseases associated with yeast or fungi or proliferative disorders, such  
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds  
 CC or polypeptides, or the genetically modified organism are useful for  
 CC preparing a medicament for modifying the endogenous flora of humans and  
 CC other mammals. The vaccine is useful for immunising against yeast or  
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,  
 CC ischaemia, diseases related with viral infections or neurodegenerations.  
 CC This sequence represents a polynucleotide associated with the Bax gene  
 CC described in the disclosure of the invention

XX SQ Sequence 15790 BP; 5181 A; 2570 C; 2199 G; 5840 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2.25 Length: 15790  
 Score: 72.00 Matches: 12  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 87.80% Indels: 0  
 DB: 6 Gaps: 0

US-09-976-740-19 (1-15) x ABQ76615 (1-15790)

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Search completed: March 12, 2004, 21:08:29  
 Job time : 31.776 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 20:05:17 ; Search time 5.08568 Seconds  
(without alignments)  
1636.805 Million cell updates/sec

Title: US-09-976-740-19  
Perfect score: 82  
Sequence: 1 EEEEDDEDEDEDD 15

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	82	100.0	45	4	US-09-517-849-30
3	82	100.0	45	4	US-09-616-289-30
4	82	100.0	78	4	US-08-979-608A-31
5	82	100.0	78	4	US-08-517-849-31
6	82	100.0	78	4	US-09-616-289-31
7	82	100.0	1208	4	US-08-979-608A-16
8	82	100.0	1208	4	US-09-517-849-16
9	82	100.0	1208	4	US-09-616-289-16
10	82	100.0	1614	4	US-09-616-289-45
11	82	100.0	12425	4	US-09-616-289-50
12	73	89.0	4599	1	US-08-431-080-27

13	73	89.0	4599	2	US-08-938-534-27	Sequence 27, Appl
14	73	89.0	4599	4	US-09-345-294-27	Sequence 27, Appl
15	71	86.6	2736	4	US-09-220-132-66	Sequence 66, Appl
16	71	86.6	7585	4	US-09-418-710-22	Sequence 22, Appl
17	70	85.4	956	1	US-08-431-080-25	Sequence 25, Appl
18	70	85.4	956	1	US-08-431-080-32	Sequence 32, Appl
19	70	85.4	956	2	US-08-938-534-25	Sequence 25, Appl
20	70	85.4	956	2	US-08-938-534-32	Sequence 32, Appl
21	70	85.4	956	4	US-09-345-294-25	Sequence 25, Appl
22	70	85.4	956	4	US-09-345-294-32	Sequence 32, Appl
23	70	85.4	1194	4	US-09-220-132-31	Sequence 31, Appl
24	70	85.4	2518	3	US-09-433-699-3	Sequence 3, Appl
25	70	85.4	5751	4	US-09-023-655-1415	Sequence 1415, Ap
26	70	85.4	11907	3	US-08-061-376-4	Sequence 4, Appl
27	70	85.4	14255	1	US-08-320-559-1	Sequence 1, Appl
28	70	85.4	14255	1	US-08-327-392-1	Sequence 1, Appl
29	70	85.4	14255	3	US-08-306-691B-55	Sequence 55, Appl
30	70	85.4	14255	3	US-08-545-860D-1	Sequence 1, Appl
31	70	85.4	14255	5	PCT-US94-0446-1	Sequence 1, Appl
32	69	84.1	1275	5	US-08-552-142A-3	Sequence 3, Appl
33	69	84.1	1275	1	US-08-910-973-3	Sequence 3, Appl
34	69	84.1	1275	1	US-09-499-227-3	Sequence 3, Appl
35	69	84.1	1275	5	PCT-US95-05741-3	Sequence 3, Appl
36	69	84.1	2101	2	US-08-568-458A-9	Sequence 9, Appl
37	69	84.1	2101	2	US-08-487-826B-9	Sequence 9, Appl
38	69	84.1	2101	4	US-09-210-288-9	Sequence 9, Appl
39	69	84.1	7295	2	US-08-487-826B-15	Sequence 15, Appl
40	68	82.9	2581	4	US-09-370-836-66	Sequence 66, Appl
41	68	82.9	3164	4	US-09-023-655-816	Sequence 16, App
42	68	82.9	3489	2	US-08-728-323A-1	Sequence 1, Appl
43	68	82.9	3489	4	US-09-298-568-1	Sequence 1, Appl
44	68	82.9	3489	4	US-09-410-399-1	Sequence 1, Appl
45	68	82.9	32207	2	US-08-770-379-20	Sequence 20, Appl

## ALIGNMENTS

RESULT 1  
US-08-979-608A-30  
; Sequence 30, Application US/08979608A  
; Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-NOV-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...45  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-08-979-608A-30

Alignment Scores:  
Pred. No.: 4.28e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-976-740-19 (1-15) x US-08-979-608A-30 (1-45)  
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DB 1 GAAGAGAGAGATGATGATGATGAAGTGAAGTGAAGATGAT 45

RESULT 2  
US-09-517-849-30  
Sequence 30, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-8906  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...45  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-517-849-30

Alignment Scores:  
Pred. No.: 4.28e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-976-740-19 (1-15) x US-09-517-849-30 (1-45)  
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RESULT 3  
US-09-616-289-30  
Sequence 30, Application US/09616289  
Patent No. 6632823  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-30

Alignment Scores:  
Pred. No.: 4.28e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-19 (1-15) x US-09-616-289-30 (1-45)  
QY 1 GUGUGUGUASPAPAPGUAAPGUAAPGUGUASPASP 15  
DB 1 GAAGAGAGAGATGATGATGATGAAGTGAAGTGAAGATGAT 45

RESULT 4  
US-08-979-608A-31  
Sequence 31, Application US/08979608A  
Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/08/979,608  
FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-08-979-608A-31

Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-Mar-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3963/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-08-979-608A-31  
Alignment Scores:  
Pred. No.: 7.31e-05 Length: 78  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-19 (1-15) x US-08-979-608A-31 (1-78)  
QY 1 GUGUGUGUUAAPASPAGUASPGLUASPGLUASPGLUASPASP 15  
DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45  
RESULT 5  
US-09-517-849-31  
Sequence 31, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-517-849-31  
Alignment Scores:  
Pred. No.: 7.31e-05 Length: 78  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-19 (1-15) x US-09-517-849-31 (1-78)  
QY 1 GUGUGUGUUAAPASPAGUASPGLUASPGLUASPGLUASPASP 15  
DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 45  
RESULT 6  
US-09-616-289-31  
Sequence 31, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
AND TREATING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03





US-09-976-740-19 (1-15) x US-09-517-849-16 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPGIIUAAPGIIUAAPGIIUAAP 15  
DB 22 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 66

RESULT 9

US-09-616-289-16  
Sequence 16, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-09-616-289-16

Alignment Scores:

Pred. No.: 0.00105 Length: 1208  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-19 (1-15) x US-09-616-289-16 (1-1208)

QY 1 GIUGIUGIUGIUAASPAPGIIUAAPGIIUAAPGIIUAAP 15  
DB 22 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 66

RESULT 10

US-09-616-289-45  
Sequence 45, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/031,930

PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 45  
LENGTH: 1614  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1614)  
US-09-616-289-45

Alignment Scores:

Pred. No.: 0.0014 Length: 1614  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-19 (1-15) x US-09-616-289-45 (1-1614)

QY 1 GIUGIUGIUGIUAASPAPGIIUAAPGIIUAAPGIIUAAP 15  
DB 985 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 1029

RESULT 11

US-09-616-289-50  
Sequence 50, Application US/09616289  
Patent No. 6632923  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.

APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 50  
LENGTH: 12425  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-50

Alignment Scores:

Pred. No.: 0.0102 Length: 12425  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-976-740-19 (1-15) x US-09-616-289-50 (1-12425)

QY 1 GIUGIUGIUGIUAASPAPGIIUAAPGIIUAAPGIIUAAP 15  
DB 4238 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 4282

```

RESULT 12
US-08-431-080-27
; Sequence 27, Application US/08431080
; Patent No. 569686
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,080
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SN 08/326,781
; FILING DATE: October 20, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: ARCD:155/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4599 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-431-080-27

Alignment Scores:
Pred. No.:          0.0688      Length:         4599
Score:              73.00       Matches:        12
Percent Similarity: 100.00%     Conservative:   3
Best Local Similarity: 80.00%    Mismatches:    0
Query Match:        89.02%       Indels:        0
DB:                 1           Gaps:          0

US-09-976-740-19 (1-15) X US-08-431-080-27 (1-4599)

QY      1  GUUGUUGUUGUAASPAGSPGUAAPGUAAPGUGUUAASP 15
Dd      1231 GAAGAAGAGATGATGCACGAACGACGACGACGATGAT 1275

RESULT 13
US-08-938-534-27
; Sequence 27, Application US/08938534
; Patent No. 5916752
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston

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1 STATE: TEXAS
2 COUNTRY: UNITED STATES OF AMERICA
3 ZIP: 77210
4
5 COMPUTER READABLE FORM:
6
7 MEDIUM TYPE: floppy disk
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9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
11 SOFTWARE: Patentin Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/938,534
15 FILING DATE: 26-SEP-1997
16
17 CLASSIFICATION: 536
18
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/431,080
21
22 FILING DATE:
23
24 APPLICATION NUMBER: SN 08/326,781
25 FILING DATE: October 20, 1994
26
27 ATTORNEY/AGENT INFORMATION:
28
29 NAME: Parker, David L.
30 REGISTRATION NUMBER: 32,165
31 REFERENCE/DOCKET NUMBER: ARCD:155/PAR
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (512) 418-3000
34 TELEFAX: (713) 789-2679
35
36 TELEX: 79-0924
37
38 INFORMATION FOR SEQ ID NO: 27:
39
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 4599 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45
46 US-08-938-534-27
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49
50 Alignment Scores:
51 Pred. No.: 0.0688 Length: 4599
52 Score: 73.00 Matches: 12
53 Percent Similarity: 100.00% Conservative: 3
54 Best Local Similarity: 80.00% Mismatches: 0
55 Query Match: 89.02% Indels: 0
56 DB: 2 Gaps: 0
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60 US-09-976-740-19 (1-15) x US-08-938-534-27 (1-4599)
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APPLICATION NUMBER: 08/431,080  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parker, David L.  
 REGISTRATION NUMBER: 32,165  
 REFERENCE/DOCKET NUMBER: ARCD:155/PAR  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (713) 789-2679  
 TELEX: 79-0924  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4599 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
 US-09-345-294-27

Alignment Scores:  
 Pred. No.: 0.0688 Length: 4599  
 Score: 73.00 Matches: 12  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 89.02% Indels: 0  
 DB: 4 Gaps: 0

US-09-976-740-19 (1-15) \* US-09-345-294-27 (1-4599)

OY 1 Glugluglugluaspaspaspgluaspgluaspgluaspasp 15  
 Db 1231 GAAGAGAGAGATGATGACGACGACGACGATGATGAT 1275

RESULT 15  
 US-09-220-132-66  
 Sequence 66, Application US/09220132  
 Patent No. 6506607  
 GENERAL INFORMATION:  
 APPLICANT: Shyjan, Andrew W.  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT  
 FILE REFERENCE: 07334-074001  
 CURRENT APPLICATION NUMBER: US/09/220,132  
 PRIOR FILING DATE: 1998-12-23  
 PRIOR APPLICATION NUMBER: US 60/079,303  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: US 60/068,821  
 PRIOR FILING DATE: 1997-12-24  
 NUMBER OF SEQ ID NOS: 191  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 66  
 LENGTH: 2736  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-220-132-66

Alignment Scores:  
 Pred. No.: 0.0786 Length: 2736  
 Score: 71.00 Matches: 12  
 Percent Similarity: 100.00% Conservative: 3  
 Best Local Similarity: 80.00% Mismatches: 0  
 Query Match: 86.59% Indels: 0  
 DB: 4 Gaps: 0

US-09-976-740-19 (1-15) \* US-09-220-132-66 (1-2736)

OY 1 Glugluglugluaspaspaspgluaspgluaspgluaspasp 15  
 Db 1325 GAAGAGAGAGATGATGACGATGATGATGATGATGATGAT 1369

Search completed: March 13, 2004, 04:06:22  
 Job time : 9.08568 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

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Run on:      March 12, 2004, 20:46:42 ; Search time 21.7013 Seconds
              (without alignments)
              2544.725 Million cell updates/sec
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Perfect score: 82
Sequence: 1 EEEEDDDDEDEDEDD 15
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Scoring table:		BLOSUM62
Xgapop	10.0	Xgapext 0.5
Ygapop	10.0	Ygapext 0.5
Fgapop	6.0	Fgapext 7.0
Delop	6.0	Delext 7.0

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Searched:      2432557 segs, 1840798884 residues
Total number of hits satisfying chosen parameters: 4865114
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Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing:
  Minimum Match 0%
  Maximum Match 100%
Listing first 45 summaries

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Command line parameters:
-MODEL=5rname+ p2n.model -DEV=xip
-Q/cgml2 1VSUFO.spool.p/USO9976740/funat 10032004_094549.19588/abp query.fasta_1.18988
-D=Published Applications NA -QEXT=fastad -SUFFIX=rmpb -MIMATCH=0.1
-LOOPC=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsnum62
-TRANS=humana0.cdd -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfco -NOR=exlc -HEA5T5E=100 -MINLEN=0
-NCLEN=2000000000 -USER=USO9976740 -QCGN_1_1_712 @runat_10032004_094549.19588
-WALK=6 -ICF=05 -NO_MSAE -LARGEQUERY -NEG_SCORES=0 -WAIT -DSB3LOCK=100
-FLAGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THEAD=10 -XGAPOP=6 -XGAEXT=0.5
-XGAPOP=6 -FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELEXT=7

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Database :
PublishedApplications/NM:*
1: /cgn2_6/prodata/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/1/pubna/PCr_NEM_PUB.seq.*
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5: /cgn2_6/prodata/1/pubna/US07_NEM_PUB.seq.*
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10: /cgn2_6/prodata/1/pubna/US09_PUBCOMB.seq.*
11: /cgn2_6/prodata/1/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/prodata/1/pubna/US09C_NEM_PUB.seq.*
13: /cgn2_6/prodata/1/pubna/US10A_PUBCOMB.seq.*
14: /cgn2_6/prodata/1/pubna/US10B_PUBCOMB.seq.*
15: /cgn2_6/prodata/1/pubna/US10C_PUBCOMB.seq.*
16: /cgn2_6/prodata/1/pubna/US10C_NEM_PUB.seq.*
17: /cgn2_6/prodata/1/pubna/US60_NEM_PUB.seq.*
18: /cgn2_6/prodata/1/pubna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	82	100.0	45	9	US-09-962-055-30	Sequence 30, App1
2	82	100.0	45	9	US-09-976-740-30	Sequence 30, App1
3	82	100.0	45	12	US-10-671-542-30	Sequence 30, App1
4	82	100.0	45	13	US-10-023-529-30	Sequence 30, App1
5	82	100.0	45	13	US-10-023-523-30	Sequence 30, App1
6	82	100.0	45	13	US-10-616-187-30	Sequence 30, App1
7	82	100.0	78	9	US-09-962-055-31	Sequence 31, App1
8	82	100.0	78	9	US-09-976-740-31	Sequence 31, App1
9	82	100.0	78	12	US-10-671-542-31	Sequence 31, App1
10	82	100.0	78	13	US-10-023-529-31	Sequence 31, App1
11	82	100.0	78	13	US-10-023-523-31	Sequence 31, App1
12	82	100.0	78	15	US-10-616-187-31	Sequence 31, App1
13	82	100.0	1208	9	US-09-962-055-16	Sequence 16, App1
14	82	100.0	1208	9	US-09-976-740-16	Sequence 16, App1
15	82	100.0	1208	12	US-10-671-542-16	Sequence 16, App1
16	82	100.0	1208	13	US-10-023-529-16	Sequence 16, App1
17	82	100.0	1208	13	US-10-023-523-16	Sequence 16, App1
18	82	100.0	1208	15	US-10-616-187-16	Sequence 16, App1
19	82	100.0	1336	14	US-10-102-806-447	Sequence 247, App1
20	82	100.0	1445	10	US-09-945-527-6	Sequence 6, App1
21	82	100.0	1514	9	US-09-976-740-45	Sequence 45, App1
22	82	100.0	1514	12	US-10-671-542-45	Sequence 45, App1
23	82	100.0	1514	13	US-10-023-529-45	Sequence 45, App1
24	82	100.0	1514	13	US-10-023-523-45	Sequence 45, App1
25	82	100.0	1514	15	US-10-616-187-45	Sequence 45, App1
26	82	100.0	12425	9	US-09-976-740-50	Sequence 50, App1
27	82	100.0	12425	12	US-10-671-542-50	Sequence 50, App1
28	82	100.0	12425	13	US-10-023-529-50	Sequence 50, App1
29	82	100.0	12425	13	US-10-023-523-50	Sequence 50, App1
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31	75	91.5	1474	12	US-10-425-114-4967	Sequence 14967, App1
32	75	91.5	1587	9	US-10-424-559-29792	Sequence 29792, App1
33	72	87.8	932	9	US-09-976-740-55	Sequence 55, App1
34	72	87.8	932	12	US-10-425-114-33034	Sequence 13034, App1
35	72	87.8	1284	14	US-10-032-585-6386	Sequence 6386, App1
36	71	86.6	397	12	US-10-424-559-85863	Sequence 85863, App1
37	71	86.6	454	9	US-09-980-107-2462	Sequence 2462, App1
38	71	86.6	454	9	US-09-954-531-1094	Sequence 1094, App1
39	71	86.6	913	12	US-10-424-559-77101	Sequence 77101, App1
40	71	86.6	2142	15	US-09-917-800A-1567	Sequence 1567, App1
41	71	86.6	2142	15	US-10-131-803-55	Sequence 35, App1
42	71	86.6	2142	15	US-10-131-996A-20	Sequence 20, App1
43	71	86.6	2142	15	US-10-131-996A-20	Sequence 20, App1
44	70	85.4	231	12	US-10-072-012-741	Sequence 241, App1
45	70	85.4	231	15	US-10-085-783A-7014	Sequence 7014, App1
					US-10-242-535A-7014	Sequence 7014, App1

## ALIGNMENTS

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RESULT 1
US-09-962-055-30
; Sequence 30, Application US/09962055
; Patent No. US20020052033A1
; GENERAL INFORMATION:
;

```

APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arlona, Anibal A.

TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Fish & Richards  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 45 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...45  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-09-962-055-30  
Alignment Scores:  
Pred. No.: 4,47e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-976-740-19 (1-15) x US-09-962-055-30 (1-45)  
Cy 1 GUGUUGUUGUUAASPAPSPGUAASPGUUAASPGUUAASPA 15  
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 45  
RESULT 2  
US-09-976-740-30  
Sequence 30, Application US/09976740  
Publication No. US20020194633A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/976,740  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-976-740-30

Alignment Scores:  
Pred. No.: 4,47e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-976-740-19 (1-15) x US-09-976-740-30 (1-45)  
Cy 1 GUGUUGUUGUUAASPAPSPGUAASPGUUAASPGUUAASPA 15  
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 45  
RESULT 3  
US-10-671-242-30  
Sequence 30, Application US/10671242  
Publication No. US20040040049A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/671,242  
CURRENT FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-671-242-30  
Alignment Scores:  
Pred. No.: 4,47e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0  
US-09-976-740-19 (1-15) x US-10-671-242-30 (1-45)  
Cy 1 GUGUUGUUGUUAASPAPSPGUAASPGUUAASPGUUAASPA 15  
Db 1 GAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGATGAT 45  
RESULT 4  
US-10-023-529-30  
Sequence 30, Application US/10023529  
Publication No. US20020129388A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
CURRENT FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-529-30

FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,529  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-529-30

Alignment Scores:  
Pred. No.: 4,47e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-529-30 (1-45)

Cy 1 GluGluGluGluAspAspGluAspGluGluGluAspAsp 15  
Db 1 GAAGAGGAAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 5  
US-10-023-523-30  
Sequence 30, Application US/10023523  
Publication No. US20020152485A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/023,523  
CURRENT FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-023-523-30

Alignment Scores:  
Pred. No.: 4,47e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-09-976-740-19 (1-15) x US-10-023-523-30 (1-45)

Cy 1 GluGluGluGluAspAspGluAspGluGluGluAspAsp 15  
Db 1 GAAGAGGAAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 6  
US-10-616-187-30  
Sequence 30, Application US/10616187  
Publication No. US20040013668A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/616,187  
CURRENT FILING DATE: 2003-07-09  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 30  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-616-187-30

Alignment Scores:  
Pred. No.: 4,47e-05 Length: 45  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 15 Gaps: 0

US-09-976-740-19 (1-15) x US-10-616-187-30 (1-45)

Cy 1 GluGluGluGluAspAspGluAspGluGluGluAspAsp 15  
Db 1 GAAGAGGAAGAGATGATGATGAAGATGAAGATGAAGATGAT 45

RESULT 7  
US-09-962-055-31  
Sequence 31, Application US/09962055  
Patent No. US20020052033A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston

STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-8070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-962-055-31  
Alignment Scores:  
Pred. No.: 7,45e-05 Length: 78  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-976-740-19 (1-15) x US-09-962-055-31 (1-78)  
QY 1 GUGUGUGUUAASPAPSPGUAASPGUUAASPGUUAASPP 15  
DB 1 GAAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 45  
RESULT 8  
US-09-976-740-31  
Sequence 31, Application US/09976740  
Publication No. US20020194633A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/976,740  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53

SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 31  
LENGTH: 78  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-976-740-31  
Alignment Scores:  
Pred. No.: 7,45e-05 Length: 78  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-976-740-19 (1-15) x US-09-976-740-31 (1-78)  
QY 1 GUGUGUGUUAASPAPSPGUAASPGUUAASPGUUAASPP 15  
DB 1 GAAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 45  
RESULT 9  
US-10-671-242-31  
Sequence 31, Application US/10671242  
Publication No. US20040040049A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
APPLICANT: Lees, Robert S.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/671,242  
CURRENT FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 31  
LENGTH: 78  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-671-242-31  
Alignment Scores:  
Pred. No.: 7,45e-05 Length: 78  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0  
US-09-976-740-19 (1-15) x US-10-671-242-31 (1-78)  
QY 1 GUGUGUGUUAASPAPSPGUAASPGUUAASPGUUAASPP 15  
DB 1 GAAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 45  
RESULT 10  
US-10-023-529-31  
Sequence 31, Application US/10023529  
Publication No. US20020129388A1  
GENERAL INFORMATION:



```

; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT FILING DATE: US/10/023,529
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-023-529-31

Alignment Scores:
Pred. No.: 7,45e-05 Length: 78
Score: 82.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13

US-09-976-740-19 (1-15) x US-10-023-529-31 (1-78)

Cy 1 GluGluglGluGluAspAspGluAspGluAspGluGluAspAsp 15
Db 1 GAAGAGGAAGAGATGATGATGAGATGAGATGAGATGAGATGAT 45

RESULT 11
US-10-023-523-31
; Sequence 31, Application US/10023523
; Publication No. US20020152485A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT FILING DATE: US/10/023,523
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US/09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 08/979,608
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: US 60/031,930
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 60/048,547
; PRIOR FILING DATE: 1997-06-03
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 78
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```

US-10-023-523-31

Alignment Scores:
Pred. No.: 7,45e-05 Length: 78
Score: 82.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 13

US-09-976-740-19 (1-15) x US-10-616-187-31 (1-78)

Cy 1 GluGluglGluGluAspAspGluAspGluAspGluGluAspAsp 15
Db 1 GAAGAGGAAGAGATGATGATGAGATGAGATGAGATGAGATGAT 45

RESULT 13
US-09-962-055-16
; Sequence 16, Application US/09362055
; Patent No. US20020052033A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
```

BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS

NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/962,055  
FILING DATE: 24-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/579,608  
FILING DATE: 26-NOV-1997  
APPLICATION NUMBER: US 60/031,930  
FILING DATE: 27-NOV-1996

ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1208 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...651  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-962-055-16

Alignment Scores:  
Pred. No.: 0.000956 Length: 1208  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-976-740-19 (1-15) x US-09-962-055-16 (1-1208)

QY 1 GUGUGUGUGUASPAPSPGUAAPGUAAPGUGUASPASP 15  
DB 22 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 66

RESULT 14  
US-09-976-740-16  
Sequence 16, Application US/09976740  
Publication No. US20020194633A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/976,740  
FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 09/616,289  
PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-10-671-242-16

Alignment Scores:  
Pred. No.: 0.000956 Length: 1208  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0

US-09-976-740-19 (1-15) x US-09-976-740-16 (1-1208)

QY 1 GUGUGUGUGUASPAPSPGUAAPGUAAPGUGUASPASP 15  
DB 22 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 66

RESULT 15  
US-10-671-242-16  
Sequence 16, Application US/10671242  
Publication No. US2004004049A1  
GENERAL INFORMATION:  
APPLICANT: Lees, Robert S.  
APPLICANT: Lees, Ann M.  
APPLICANT: Law, Simon W.  
APPLICANT: Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
TITLE OF INVENTION: ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/10/671,242  
FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: US/09/616,289  
PRIOR FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 1208  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-10-671-242-16

Alignment Scores:  
Pred. No.: 0.000956 Length: 1208  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

US-09-976-740-19 (1-15) x US-10-671-242-16 (1-1208)

QY 1 G|uG|uG|uG|uA|sP|sP|sP|uA|sP|uA|sP|uG|uA|sP|sP| 15  
DB 22 GAAAGGAAAGAAATGATGATGAAATGAAATGAAATGAAAGATGAT 66

Search completed: March 13, 2004, 04:26:13  
Job time : 23.7013 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004. CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:55:37 ; Search time 226.799 Seconds

(without alignments)  
1975.018 Million cell updates/sec

Title: US-09-976-740-19  
Perfect score: 82  
Sequence: 1 EEEEDDEDEDEDD 15

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seg length: 0  
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model DEV=xip  
-Q=/cgm2\_1/USPTO.spool/p/US09976740/runat\_10032004\_094548\_19551/app.query.fasta\_1.1898  
-DB=EST-QPMT=fastlap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USRR=US09976740 @CGN 1.1 10233 @runat\_10032004\_094548\_19551 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGESQUTRY -NES\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_esttm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_hiv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vtc:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_fam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_prc:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	82	100.0	171	9	AA807448
2	82	100.0	200	9	BB504871
3	82	100.0	204	9	AA481545
4	82	100.0	241	9	AT742585
5	82	100.0	244	9	AA481527
6	82	100.0	271	9	AA765474
7	82	100.0	274	12	BI004562
8	82	100.0	275	9	AA806888
9	82	100.0	278	9	AA810871
10	82	100.0	284	9	AA766034
11	82	100.0	302	10	BF194967
12	82	100.0	322	9	AI470106
13	82	100.0	324	10	BF806978
14	82	100.0	326	9	AA815219
15	82	100.0	345	10	BF941758
16	82	100.0	367	9	AA769505
17	82	100.0	383	10	AA845391
18	82	100.0	384	9	AA836383
19	82	100.0	397	10	AA594381
20	82	100.0	412	10	AA134620
21	82	100.0	429	9	AI097526
22	82	100.0	446	9	AI379283
23	82	100.0	451	9	AA016794
24	82	100.0	455	9	AI186873
25	82	100.0	460	9	AA054879
26	82	100.0	461	9	AI921818
27	82	100.0	466	10	BF061129
28	82	100.0	467	9	AI819090
29	82	100.0	472	9	AI961519
30	82	100.0	472	9	AA827095
31	82	100.0	480	9	AI886859
32	82	100.0	483	9	AI569682
33	82	100.0	487	9	AI186705
34	82	100.0	495	9	AI199022
35	82	100.0	501	9	AI796089
36	82	100.0	509	9	AI632586
37	82	100.0	512	10	AA515766
38	82	100.0	518	10	BE269536
39	82	100.0	572	12	BE697252
40	82	100.0	580	10	BE257093
41	82	100.0	583	9	AI660679
42	82	100.0	590	9	AI123580
43	82	100.0	593	9	AI928488
44	82	100.0	680	10	BE675122
45	82	100.0	683	10	BE857936

# ALIGNMENTS

RESULT 1  
AA807448  
LOCUS AA807448  
DEFINITION n65b12.s1 NCI\_CGAP GCBI Homo sapiens cDNA clone IVAGB:123465 3'  
similar to contains element MBR22 repetitive element ;, mRNA  
sequence.  
ACCESSION AA807448  
VERSION AA807448.1 GI:2877024  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 171)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[www.bio.linnl.gov/birop/image/image.html](http://www.bio.linnl.gov/birop/image/image.html)  
Insert length: 1069 Std Error: 0.00  
Seq primer: -40ml3 fwd. RT from Amersham  
High quality sequence stop: 158.  
Location/Qualifiers  
1. 171  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1234655"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP GCBI"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI). Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
[5'-TGTTACCATCTGAGAGCGAGCGCCCTCATTTTCTTTT-3'  
]. Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.:	0.264	Length:	171
Score:	82.00	Matches:	15
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-19 (1-15) x AA807448 (1-171)

Qy 1 GUGUGUGUGUASPAPSPAGUASPGLUASPGLUASPASP 15

DB 103 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 147

RESULT 2  
BE504871  
LOCUS BE504871 200 bp mRNA linear EST 04-AUG-2000  
DEFINITION h333905.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3209816 3'  
similar to contains element TARI repetitive element ;, mRNA  
sequence.  
ACCESSION BE504871  
VERSION BE504871.1 GI:9707279  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 200)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:  
[info@image.linnl.gov](mailto:info@image.linnl.gov)  
Seq primer: -40UP from Glibco  
High quality sequence stop: 139.  
Location/Qualifiers  
1. 200  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3209816"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP GC6"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA  
from the normalized library NCI CGAP GC4 was prepared, and  
as circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneids  
1257096-1258631, 1469064-1470983, and 1475592-1476743).  
Subtraction by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.:	0.31	Length:	200
Score:	82.00	Matches:	15
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-09-976-740-19 (1-15) x BE504871 (1-200)

Qy 1 GUGUGUGUGUASPAPSPAGUASPGLUASPGLUASPASP 15

DB 132 GAAGAGGAGAGATGATGATGAAGATGAAGATGAAGATGAT 176

RESULT 3  
AA481545  
LOCUS AA481545 204 bp mRNA linear EST 14-AUG-1997  
DEFINITION aa35906.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:815290 3'  
similar to contains element MER6 repetitive element ;, mRNA  
sequence.  
ACCESSION AA481545  
VERSION AA481545.1 GI:2211097  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 204)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Possible reversed clone: polyT not found  
 Seq primer: -41m13 fwd. ET from Amersham  
 High quality sequence stop: 203.

## FEATURES

## source

Location/Qualifiers

1..204

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:6034387"

/db\_xref="taxon:9606"

/clone="IMAGE:815290"

/tissue\_type="germinal center B cell"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GCBI"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD+),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo (dT) primer

[5'-TGTTACCAATCGAAGGAGGAGCGCGCTATTTTTTTTTTTT-3'

] Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.: 0.316 Length: 204  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-976-740-19 (1-15) x AA481545 (1-204)

QY 1 GUGUGUGUGUAASPASPAGUAAPGUAAPGUGUAASP 15

DB 104 GAAGGAGAAAGATGATGATGAAGATGAAGATGAAGATGAT 148

## RESULT 4

## LOCUS

## DEFINITION

AI742585 241 bp mRNA linear EST 19-DEC-1999  
 W55907.x1 Soares NSF P8.9W OT PA.P S1 Homo sapiens CDNA clone  
 IMAGE:2369052.3' similar to contains TAR1.b2 TAR1 TAR1 repetitive  
 element; mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
 Insert Length: 901 Scd Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 225.

## FEATURES

## source

Location/Qualifiers

1..241

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2369052"

/lab\_host="DH10B"

/clone\_lib="Soares NSF P8.9W OT PA.P S1"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker. Site 1: Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and as circles were used in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and cloneids: Soares NBHSF pool 1:

309384-310919, 323208-325895, Soares NB2HP pool 1:

145002-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HP-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

344776-306311, 320136-322823, 326280-326663 Soares NBHOT

pool 1: 723720-726407, 739080-740599 Subtraction by Bento

Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.: 0.375 Length: 241  
 Score: 82.00 Matches: 15  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-976-740-19 (1-15) x AI742585 (1-241)

QY 1 GUGUGUGUGUAASPASPAGUAAPGUAAPGUGUAASP 15

DB 176 GAAGGAGAAAGATGATGATGAAGATGAAGATGAAGATGAT 220

## RESULT 5

## LOCUS

## DEFINITION

AA481527 244 bp mRNA linear EST 14-AUG-1997  
 aa35606.s1 NCI CGAP GCBI Homo sapiens CDNA clone IMAGE:815266.3'  
 similar to contains element MSRI repetitive element; mRNA  
 sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
 Ph.D., Gerald Marti, M.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Possible reversed clone: polyT not found  
 Seq primer: -41m13 fwd. ET from Amersham  
 High quality sequence stop: 243.





## High quality sequence stop: 274.

FEATURES  
Location/Qualifiers

1..274  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_str="Adult"  
/clone\_id="HN0054"  
/note="Organ: head normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Alignment Scores:  
Pred. No.: 0.428 Length: 274  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-09-976-740-19 (1-15) x B1004562 (1-274)

Qy 1 GluGluGluGluAspAspAspGluAspGluAspGluAspAsp 15  
|||||  
Db 251 GAGAGGAGAGAGATGATGATGAGATGAGATGAGATGATGAT 207

RESULT 8 275 bp mRNA linear EST 07-APR-1998  
AA806888  
LOCUS ob64g05.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:1351450 3'  
DEFINITION similar to contains element TARI repetitive element ;, mRNA  
sequence.

ACCESSION AA806888  
VERSION AA806888.1 GI:2876464  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 275)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.lnl.gov/bdrrp/image/image.html](http://www-bio.lnl.gov/bdrrp/image/image.html)

Insert Length: 1112 Std Error: 0.00  
Seg primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 229.  
Location/Qualifiers

## FEATURES

source

1..275  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_id="IMAGE:1351450"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP GCBI"  
/note="Vector: pRT73D-Pac (Pharmacia) with a modified  
germinal center B cells by flow sorting (CD20+, IgD-),

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),  
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman  
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was  
primed with a Not I - oligo(dT) primer  
15'-TGTTACCATCTGAGTGGGCGCGCCCTCATTTTTTTTTTTT-3'  
). Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pRT73 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
Pred. No.: 0.43 Length: 275  
Score: 82.00 Matches: 15  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-976-740-19 (1-15) x AA806888 (1-275)

Qy 1 GluGluGluGluAspAspAspGluAspGluAspGluAspAsp 15  
|||||  
Db 85 GAGAGGAGAGAGATGATGATGAGATGAGATGAGATGATGAT 129

RESULT 9 278 bp mRNA linear EST 19-FEB-1998  
AA810871  
LOCUS ob64g05.s1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:136184 3'  
DEFINITION similar to contains element PTK7 repetitive element ;, mRNA  
sequence.

ACCESSION AA810871  
VERSION AA810871.1 GI:2880482  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 278)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,  
Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.lnl.gov/bdrrp/image/image.html](http://www-bio.lnl.gov/bdrrp/image/image.html)

Insert Length: 1143 Std Error: 0.00  
Seg primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 269.  
Location/Qualifiers

## FEATURES

source

1..278  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_id="IMAGE:136184"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP GCBI"  
/note="Vector: pRT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was prepared from human tonsillar cells enriched for  
germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAGTGGAGCGGCCCTCATTTTTTTTTTTT-3' (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

##### Alignment Scores:

Pred. No.:	0.435	Length:	278
Score:	82.00	Matches:	15
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-19 (1-15) x AA810871 (1-278)

Qy 1 GIUGLUGLUGUASPAPSPGUAAPGUAAPGUAAPSP 15

Db 82 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 126

RESULT 10 284 bp mRNA linear EST 08-FEB-1998  
AA766034 0a15b09.s1 NCI CGAP CGB1 Homo sapiens cDNA clone IMAGE:1105017 3' sequence.

#### DEFINITION

similar to contains element MER22 repetitive element ;, mRNA

AA766034 GI:2817272

#### ACCESSION

AA766034.1 GI:2817272

#### KEYWORDS

Homo sapiens (human)

#### SOURCE

Homo sapiens

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

#### REFERENCE

1 (bases 1 to 284) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

#### AUTHORS

Unpublished (1997) National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

#### JOURNAL

Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU at:

www-bio.llnl.gov/bdrp/image/image.html

Insert length: 1100 Std Error: 0.00

Seq primer: -40ml3 fwd. RT from Amersham

High quality sequence stop: 283.

Location/Qualifiers

1..284

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1305017"

/tissue\_type="germinal center B cell"

/lab\_host="DH10B"

/clone\_idb="NCI CGAP CGB1"

/notes="Vector: pTV3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer

[5'-TGTACCAATCTGAGTGGAGCGGCCCTCATTTTTTTTTTTT-3' (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

##### Alignment Scores:

Pred. No.:	0.445	Length:	284
Score:	82.00	Matches:	15
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-976-740-19 (1-15) x AA766034 (1-284)

Qy 1 GIUGLUGLUGUASPAPSPGUAAPGUAAPGUAAPSP 15

Db 81 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGAT 125

RESULT 11

BF194967 7091b05.x1 NCI CGAP Cyl8 Homo sapiens cDNA clone IMAGE:3643712 3' sequence.

BF194967 similar to contains element TARI TARI repetitive element ;, mRNA

#### DEFINITION

BF194967 302 bp mRNA linear EST 03-NOV-2000

#### LOCUS

BF194967 GI:11081346

#### ACCESSION

BF194967

#### KEYWORDS

Homo sapiens (human)

#### SOURCE

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

#### REFERENCE

1 (bases 1 to 302) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

#### AUTHORS

#### JOURNAL

#### COMMENT

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU, send email to: info@image.llnl.gov.

Location/Qualifiers

1..302

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3643712"

/tissue\_type="fibrocyte"

/lab\_host="DH10B (phage-resistant)"

/clone\_idb="NCI CGAP Cyl8"

/notes="Organ: Ovary; Vector: pTV3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAGTGGAGCGGCCCTCATTTTTTTTTTTT-3' (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

##### Alignment Scores:

Pred. No.:	0.474	Length:	302
Score:	82.00	Matches:	15





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:49:56 ; Search time 394.901 Seconds

(without alignments)  
2853.675 Million cell updates/sec

Title: US-09-976-740-20

Perfect score: 136

Sequence: 1 EEEDEDEDEDEDDVSEGESEVPSD 26

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/cgn2\_1/USPRO.spool.p/US09976740/runat.10032004.094548.19540/app.query.fasta\_1.1898  
-DB=Genembl -OFMT=fastap -SUFFIX=rgc -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blom62 -TRANS=human40.cdd -LIST=45  
-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976740.@CGN\_1\_1\_9705.@runat.10032004.094548.19540 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERRY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database :

1: Genembl.\*  
2: gb\_ba.\*  
3: gb\_hcg.\*  
4: gb\_in.\*  
5: gb\_om.\*  
6: gb\_ov.\*  
7: gb\_dat.\*  
8: gb\_ph.\*  
9: gb\_pl.\*  
10: gb\_pr.\*  
11: gb\_ro.\*  
12: gb\_sts.\*  
13: gb\_sy.\*  
14: gb\_un.\*  
15: gb\_vl.\*  
16: em\_da.\*  
17: em\_fun.\*  
18: em\_hum.\*  
19: em\_in.\*  
20: em\_mu.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*

29: em\_vl.\*  
30: em\_hcg\_hum.\*  
31: em\_hcg\_inv.\*  
32: em\_hcg\_other.\*  
33: em\_hcg\_mus.\*  
34: em\_hcg\_pin.\*  
35: em\_hcg\_rtd.\*  
36: em\_hcg\_mam.\*  
37: em\_hcg\_vrt.\*  
38: em\_sy.\*  
39: em\_hcgo\_hum.\*  
40: em\_hcgo\_mus.\*  
41: em\_hcgo\_other.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	136	100.0	78	6	AR199539	AR199539 Sequence
2	136	100.0	78	6	AR374691	AR374691 Sequence
3	136	100.0	78	6	AR409326	AR409326 Sequence
4	136	100.0	78	6	AX239588	AX239588 Sequence
5	136	100.0	78	6	BD056453	BD056453 Novel Low
6	136	100.0	982	6	BC007384	BC007384 Homo sapi
7	136	100.0	1208	6	AR199535	AR199535 Sequence
8	136	100.0	1208	6	AR374687	AR374687 Sequence
9	136	100.0	1208	6	AR409322	AR409322 Sequence
10	136	100.0	1208	6	AX239573	AX239573 Sequence
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12	136	100.0	1470	6	BC030129	BC030129 Homo sapi
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14	136	100.0	1614	6	AX239602	AX239602 Sequence
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17	136	100.0	12425	6	AX239607	AX239607 Sequence
18	136	100.0	237931	9	AC022098	AC022098 Homo sapi
19	116	85.3	140795	2	AC079562	AC079562 Mus muscu
20	116	85.3	218687	2	AC079501	AC079501 Mus muscu
21	108	79.4	215265	2	AC134005	AC134005 Rattus no
22	108	79.4	263957	2	AC120697	AC120697 Rattus no
23	108	79.4	279020	2	AC133803	AC133803 Rattus no
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25	104.5	76.8	84	6	AR374697	AR374697 Sequence
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31	104.5	76.8	1362	6	AR409318	AR409318 Sequence
32	104.5	76.8	1362	6	AX239569	AX239569 Sequence
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34	104.5	76.8	1422	6	AR199532	AR199532 Sequence
35	104.5	76.8	1422	6	AR374684	AR374684 Sequence
36	104.5	76.8	1422	6	AR409319	AR409319 Sequence
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38	104.5	76.8	1422	6	BD056446	BD056446 Novel Low
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42	104.5	76.8	1617	6	AX239568	AX239568 Sequence
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RESULT 1

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DEFINITION Sequence 31 from patent US 6355451.  
ACCESSION AR199539  
VERSION AR199539.1 GI:20249613  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6355451-A 31 12-MAR-2002;  
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Best Local Similarity: 100.00% Mismatches: 0  
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US-09-976-740-20 (1-26) x AR199539 (1-78)

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QY 21 GluValProGluSerAsp 26  
Db 61 GAAGTGGCCGAGAGTGAC 78

RESULT 2  
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DEFINITION Sequence 31 from patent US 6605588.  
ACCESSION AR374691  
VERSION AR374691.1 GI:40077506  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6605588-A 31 12-AUG-2003;  
FEATURES  
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Percent Similarity: 100.00% Conservative: 0  
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DB: Gaps: 0

US-09-976-740-20 (1-26) x AR374691 (1-78)

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QY 21 GluValProGluSerAsp 26  
Db 61 GAAGTGGCCGAGAGTGAC 78

RESULT 3  
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LOCUS AR409326 78 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 31 from patent US 6632923.  
ACCESSION AR409326  
VERSION AR409326.1 GI:40160114  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in  
diagnosing and treating atherosclerosis  
JOURNAL Patent: US 6632923-A 31 14-OCT-2003;  
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/organism="unknown"  
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ORIGIN  
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Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
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Query Match: 100.00% Indels: 0  
DB: Gaps: 0

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QY 21 GluValProGluSerAsp 26  
Db 61 GAAGTGGCCGAGAGTGAC 78

RESULT 4  
AX239588  
LOCUS AX239588 78 bp DNA linear PAT 26-SEP-2001  
DEFINITION Sequence 31 from Patent WO0164874.  
ACCESSION AX239588  
VERSION AX239588.1 GI:15797264  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A.  
TITLE Low density lipoprotein binding proteins and their use in diagnosing  
and treating atherosclerosis  
JOURNAL Patent: WO 0164874-A 31 07-SEP-2001;  
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Query Match: 100.00% Indels: 0

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Db	61	GAAGTCCCGAGAGTGAC	78
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LOCUS			
DEFINITION Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis,,			
ACCESSION BD056453			
VERSION JP 2001506983-A/11.			
KEYWORDS Aequorea victoria			
SOURCE Aequorea victoria			
ORGANISM Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroids; Leptomedusae; Aequoreidae; Aequorea.			
REFERENCE 1 (bases 1 to 78) Lees,A.M., Lees,R.S., Law,S.W. and Arjona,A.A. Novel low density lipoprotein binding proteins and their use in diagnosing and treating atherosclerosis Patent: JP 2001506983-A 11 29-MAY-2001; BOSTON HEART FOUNDATION INC PN JP 2001506983-A/11			
COMMENT PD 29-MAY-2001 PF 26-NOV-1997 JP 1998524870 PR 27-NOV-1996 US 60/313130, 03-JUN-1997 US 60/048547 PI ANN M LEES, ROBERT S LEES, SIMON W LAW, ANIBAL A ARJONA PC A61K38/04,A61K38/17,A61K39/00,A61K48/00,A61K49/00,A61K51/08, PC C07H21/00, PC C07K14/00,C07K14/705,C12N15/12,C12Q1/02,C12Q1/69,G01N33/566 CC			
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Db	1	GAAGGAGAAGAAATGATGATGAAGATGAAGATGAAGATGATGTGCACAGGGCTCT	60
OY	21	GIUValPProglUserASP	26
Db	61	GAAGTCCCGAGAGTGAC	78
RESULT 6 BC007384			
LOCUS			
DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone IMAGE3577194), partial cds.			
ACCESSION BC007384			
VERSION BC007384.2 GI:33988219			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 982)
AUTHORS	Straussberg,R.L., Feringold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Spemann,C.M., Schley,G.D., Altshuler,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.T., Wang,Y., Hsieh,F., Diachenko,M., Martins,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schaeetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carinci,P., Prange,C., Raba,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyar,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G., Blakesley,R.W., Touchman,A.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Gimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skaisis,U., Small, Scherer,A., Schein,U.S., Jones,S.U. and Marra,M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (baaes 1 to 982)
AUTHORS	Straussberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov On Aug 20, 2003 this sequence version replaced gi:13938477.
COMMENT	Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Rubin Laboratory CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbioology.org contact: amadan@systemsbioology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL ac: http://image.llnl.gov Series: lAL Plate: 24 Row: g Column: 10. Location/Qualifiers
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Pd	29-MAY-2001
Pf	26-NOV-1997 JP 1998524870
PR	27-NOV-1996 US 60/031930.03-JUN-1997 US 60/048547 PT
ANN M LEEBS, ROBERT S LEEBS, SIMON W LAW, ANIBAL A ARJONA PC	
A6IKX3/04,A6IKX3/17,A6IKX3/00,A6IK4B/00,A6IK49/00,A6IK51/08, PC	
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Oy	21 GUUVAIPROGUISERSAP 26
Dn	82 GAAGTGCCTCGAGATGAC 99
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DEFINITION Homo sapiens hypothetical protein BC007384, mRNA (cDNA clone IMAGE:394360), partial cds.	
ACCSSION BC030129	
VERSION BC030129.2 GI:33871478	
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1470) Krausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Bietow,K.H., Schaefer,C.F., Bhac,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heish,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schnee,E.E., Brownstein,W.U., Ustin,T.B., ToshimYuki,S., Carroll,I.P., Frange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Aranson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Guaratane,P.H., Richards,S., Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulik,S.W., Valliant,D.R., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J.T., Heathon,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shvachenko,Y., Dickson,M.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Boisford,M.C., Rodriguez,A.C., Grimmood,J., Schmutz,U., Myers,R.M., Butterfield,Y.S., Krzywinski,J.I., Skaskas,U., Smalls,D.E., Schneerich,A., Schein,J.E., Jones,S.J. and Mariz,M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16699-16903 (2002) 12437932



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Query Match: 100.00% Indels: 0
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Db 1045 GAAGTCCCGAGAGTGAC 1062

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LOCUS Homo sapiens atherin mRNA, complete cds.
ACCESSION AY453840
VERSION AY453840.1 GI:38565528
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1617)
Lees,A.M., Deconinck,A.E., Campbell,B.D. and Lees,R.S.
Atherin, a newly identified LDL-binding protein in human
atherosclerotic lesions
Unpublished
2 (bases 1 to 1617)
Deconinck,A.E., Law,S.W., Lees,R.S. and Lees,A.M.
Direct Submission
Submitted (30-OCT-2003) Harvard-MIT Division of Health Sciences and
Technology, Boston Heart Foundation, 139 Main Street, Cambridge, MA
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CDS

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ORIGIN

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 GIUVALProGIUseraap 26
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Job time : 396.901 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 19:48:14 ; Search time 41.2118 Seconds

(without alignments)  
2680.137 Million cell updates/sec

Title: US-09-976-740-20

Perfect score: 136

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Searched: 3373863 segs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0 %  
Maximum Match 100 %

Listing first 45 summaries

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-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=15  
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-USER=US09976740 -CGCN\_1\_1\_1596 -@runat\_10032004\_094547\_19532 -NCFU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: N Geneseg 29Jan04:\*

1: geneseg1980s:\*\n2: geneseg1990s:\*\n3: geneseg2000s:\*\n4: geneseg2001as:\*\n5: geneseg2001bs:\*\n6: geneseg2002s:\*\n7: geneseg2003as:\*\n8: geneseg2003bs:\*\n9: geneseg2003cs:\*\n10: geneseg2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	78	5	AAH26503
2	136	100.0	1208	2	AAV32838
3	136	100.0	1208	5	AAH26494
4	136	100.0	1336	3	AAH21860
5	136	100.0	1614	5	AAH26499
6	136	100.0	12425	5	AAH26495
7	104.5	76.8	84	5	AAH26509
8	104.5	76.8	1362	5	AAH26489

9	104.5	76.8	1422	5	AAH26490	AAH26490 Rabbit 10
10	104.5	76.8	1617	2	AAV32835	AAV32835 Rabbit 10
11	104.5	76.8	1617	5	AAH26488	AAH26488 Rabbit 10
12	104.5	76.8	2561	5	AAH26500	AAH26500 Rabbit 10
13	88	64.7	415	8	ACH46971	ACH46971 Human inf
14	88	64.7	421	8	ACH12859	ACH12859 Human inf
15	88	64.7	489	2	AAQ34771	AAQ34771 PCENP-B-1
16	88	64.7	500	8	ACH17097	ACH17097 Human adu
17	88	64.7	1446	3	AACT7994	AACT7994 Human can
18	88	64.7	1446	3	AAH33498	AAH33498 Human col
19	88	64.7	1940	5	ABA20783	ABA20783 Human ner
20	88	64.7	2633	5	ABA20784	ABA20784 Human ner
21	88	64.7	2633	2	AAQ39212	AAQ39212 CENP-B CD
22	88	64.7	2633	5	AAA64660	AAA64660 DNA encod
23	86	63.2	4712	8	ACH22667	ACH22667 Human adu
24	83.5	61.4	468	3	AACT7994	AACT7994 Human adu
25	83.5	61.4	468	3	AACT7994	AACT7994 Human adu
26	83.5	61.4	921	6	ABN99215	ABN99215 Arabidops
27	83.5	61.4	921	6	ABN99215	ABN99215 Arabidops
28	83.5	61.4	1147	3	AACT1072	AACT1072 Arabidops
29	83.5	61.4	1147	3	AACT1072	AACT1072 Arabidops
30	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
31	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
32	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
33	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
34	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
35	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
36	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
37	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
38	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
39	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
40	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
41	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
42	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
43	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
44	83	61.0	185	4	ABF80353	ABF80353 Nucleotid
45	83	61.0	185	4	ABF80353	ABF80353 Nucleotid

## ALIGNMENTS

AAH26503	AAH26503 standard; DNA; 78 BP.
AC	AAH26503;
DT	12-NOV-2001 (first entry)
DE	Low density lipoprotein binding protein (LBP) polynucleotide.
DE	Low density lipoprotein binding protein (LBP) polynucleotide.
KW	Low density lipoprotein binding protein 1; LBP-1; LDL; atherosclerosis; antiarteriosclerotic; therapy; diagnosis; vaccine; ss.
OS	Mammalia.
PN	MO200164874-A2.
PD	07-SEP-2001.
PF	28-FEB-2001; 2001WO-US006356.
PR	02-MAR-2000; 2000US-00517849.
PR	14-JUL-2000; 2000US-00616289.
PA	(BOST-) BOSTON HEART FOUND INC.
PI	Lees AM, Lees RS, Law SW, Arjona AA;
DR	WPI; 2001-565505/63.
PT	New isolated low density lipoprotein binding polypeptide for treating, diagnosing and/or identifying therapeutic agents for atherosclerosis.

XX PS Disclosure; Page 9, 143p; English.  
XX CC The present sequence is that of a polynucleotide encoding a fragment of  
CC novel low density lipoprotein binding proteins (LBP) of the invention  
CC (see AAB82797-820). LBPs are capable of binding to native and methylated  
CC low density lipoproteins (LDLs). Isolated polynucleotides encoding novel  
CC LBPs and their fragments are claimed, as well as expression vectors,  
CC cells and methods of producing the LBPs. Methods for determining if an  
CC animal is at risk for atherosclerosis, methods for evaluating an agent  
CC for use in treating atherosclerosis, and methods for treating a cell  
CC having an abnormality in structure or metabolism of LBP are also claimed,  
CC as are pharmaceutical compositions comprising an LBP polypeptide or  
CC nucleic acid, and vaccine compositions  
XX  
SQ Sequence 78 BP; 29 A; 7 C; 29 G; 13 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 1,45e-11 Length: 78  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
  
US-09-976-740-20 (1-26) x AAH26503 (1-78)  
QY 1 GUGUGUGUGUASPAPSPAPSPGUAAPGUAAPGUGUASPAPSPVPSerGUGUySer 20  
DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGCTCT 60  
QY 21 GUAUAlProGluSerASP 26  
DB 61 GAAGTCCCGAGAGCTGAC 78  
RESULT 2  
AAV32838  
ID AAV32838 standard; cDNA; 1208 BP.  
XX  
AC AAV32838;  
XX  
DT 09-NOV-1998 (first entry)  
XX  
DE Human low density lipoprotein binding protein LBP-2 cDNA.  
XX  
XX Low density lipoprotein binding protein; LDL binding protein 2; LBP-2;  
KM receptor; human; atherosclerosis; diagnosis; therapy; vaccine; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..654  
FT FT /\*tag= a  
FT FT 22..99  
FT FT /\*tag= c  
FT FT /note= "Claim 13"  
FT FT 22..66  
FT FT /\*tag= b  
FT FT /note= "Claim 12"  
FT FT 67..99  
FT FT /\*tag= d  
FT FT /note= "Claim 14"  
FT FT 622..651  
FT FT /\*tag= e  
FT FT /note= "Claim 15"  
XX  
XX MO9823282-A1.  
XX  
XX PD 04-JUN-1998.  
XX  
XX PF 26-NOV-1997; 97WO-US021857.  
XX  
XX PR 27-NOV-1996; 96US-0031930P.

PR 03-JUN-1997; 97US-0048547P.  
XX  
XX (BOST-) BOSTON HEART FOUND INC.  
XX  
XX PI Lees AM, Lees RS, Law SW, Arjona AA;  
XX  
XX DR WPI; 1998-322455/28.  
XX  
XX P-PSDB; AAM49041.  
XX  
XX Nucleic acid encoding low density lipoprotein binding proteins and  
XX related vectors - transformed cells, proteins, and modulators of binding,  
XX useful for treatment and diagnosis of atherosclerosis and for identifying  
XX subjects at risk.  
XX  
XX Claim 9; Fig 16; 47p; English.  
XX  
XX This cDNA clone codes for novel human low density lipoprotein (LDL)  
XX binding protein LBP-2 (see AAM49041). It was isolated by screening human  
XX liver, aorta and foetal brain cDNA libraries with rabbit LBP-2 cDNA. cDNA  
XX clones (see AAV32834-39) and encoded rabbit and human LBPs (see AAM49037-  
XX 42) are claimed. An abnormality in LBP metabolism or structure is  
XX diagnostic of a risk for atherosclerosis. The invention provides: methods  
XX for determining if an animal is at risk for atherosclerosis (e.g. for  
XX prenatal screening); methods for treating atherosclerosis (including gene  
XX therapy) using e.g. LBP polypeptides to bind LDL and thereby prevent  
XX formation of atherosclerotic plaque; and methods for treating a cell  
XX having an abnormality in LBP structure or metabolism. Pharmaceutical and  
XX vaccine compositions are also provided, as well as recombinant vectors  
XX and host cells used to produce recombinant LBP  
XX  
SQ Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;  
  
Alignment Scores:  
Pred. No.: 2.54e-10 Length: 1208  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
  
US-09-976-740-20 (1-26) x AAV32838 (1-1208)  
QY 1 GUGUGUGUGUASPAPSPAPSPGUAAPGUAAPGUGUASPAPSPVPSerGUGUySer 20  
DB 22 GAAGAGGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGCTCT 81  
QY 21 GUAUAlProGluSerASP 26  
DB 82 GAAGTCCCGAGAGCTGAC 99  
RESULT 3  
AAH26494  
ID AAH26494 standard; cDNA; 1208 BP.  
XX  
AC AAH26494;  
XX  
DT 12-NOV-2001 (first entry)  
XX  
DE Human low density lipoprotein binding protein 2 (LBP-2) cDNA.  
XX  
XX Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
XX atherosclerosis; antiatherosclerotic; gene therapy; diagnosis; vaccine;  
XX ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT CDS 1..654  
FT FT /\*tag= a  
FT FT /partial  
XX  
XX MO200164874-A2.

PD 07-SEP-2001.  
XX  
XX 28-FEB-2001; 2001WO-US006356.  
XX  
XX 02-MAR-2000; 2000US-00517849.  
XX 14-JUL-2000; 2000US-00616289.  
XX  
XX (BOST-) BOSTON HEART FOUND INC.  
XX  
XX Lees AM, Lees RS, Law SW, Arizona AA;  
XX WPI; 2001-565505/63.  
XX P-PSDB; AAB82803.  
XX  
XX New isolated low density lipoprotein binding polypeptide for treating,  
XX diagnosing and/or identifying therapeutic agents for atherosclerosis.  
XX  
XX Example 4; Fig 16; 143pp; English.  
XX  
XX The present sequence is that of a partial cDNA encoding novel human low  
XX density lipoprotein binding protein 2 (LBP-2, see AAB82803). Clones were  
XX isolated from human foetal brain, liver and aorta cDNA libraries using  
XX rabbit LBP-2 cDNA as probe. A full-length cDNA clone is given in  
XX AAB26499, and a genomic DNA sequence is given in AAB26495. LBP-2 nucleic  
XX acids are among claimed polynucleotides of the invention that encode  
XX novel polypeptides capable of binding to native and methylated LDL. Also  
XX claimed are isolated LBP polypeptides, and biologically active fragments  
XX of and analogues of them, as well as expression vectors, cells and methods  
XX of producing the LBPs. Methods of determining if an animal is at risk for  
XX atherosclerosis, methods for evaluating an agent for use in treating  
XX atherosclerosis, and methods for treating a cell having an abnormality in  
XX structure or metabolism of LBP are claimed. Pharmaceutical compositions  
XX comprising an LBP polypeptide or nucleic acid, and vaccine compositions,  
XX are also claimed.  
XX  
XX SO Sequence 1208 BP; 252 A; 368 C; 321 G; 266 T; 0 U; 1 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 2.54e-10 Length: 1208  
XX Score: 136.00 Matches: 26  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: Gaps: 0  
XX  
XX US-09-976-740-20 (1-26) x AAB26494 (1-1208)  
XX  
XX QY 1 GluGluGluGluAspAspGluAspGluAspGluAspValSerGluGlySer 20  
XX |||||  
XX Db 22 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGCTCT 81  
XX |||||  
XX QY 21 GluValProGluSerAsp 26  
XX |||||  
XX Db 82 GAAGTCCCGAGAGCTGAC 99  
XX |||||  
XX  
XX RESULT 4  
XX AAF21860  
XX ID AAF21860 standard; DNA; 1336 BP.  
XX  
XX AC AAF21860;  
XX XX  
XX DT 27-MAR-2001 (first entry)  
XX  
XX DE Human breast and ovarian cancer associated antigen gene SEQ ID 247.  
XX  
XX XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
XX KM neotrophic; neuroprotective; antiviral; antileukemic; hepatotropic;  
XX KM antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;  
XX KM antibacterial; antifungal; antiparasitic; cardiant; immune disorder;  
XX KM Addison's disease; allergy; autoimmune haemolytic anaemia;  
XX KM autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
KM multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KM cardiovascular disorder; wound healing; neurological disease; ds.

XX  
XX OS Homo sapiens.  
XX  
XX XX WO200055173-A1.  
XX  
XX PN 21-SEP-2000.  
XX  
XX PD 08-MAR-2000; 2000WO-US005881.  
XX  
XX PF 12-MAR-1999; 99US-0124270P.  
XX  
XX PR (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX XX Rosen CA, Ruben SM;  
XX PT WPI; 2000-611515/58.  
XX DR P-PSDB; AAB58957.  
XX  
XX PT New human breast and ovarian cancer associated gene sequences and the  
XX polypeptides encoded by these genes, useful in the prevention, treatment  
XX and diagnosis of cancer, immune disorders, cardiovascular disorders and  
XX neurological diseases.  
XX  
XX PS Claim 1; Page 670-671; 1299pp; English.  
XX  
XX CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are  
XX associated with breast and ovarian cancer. Included in the invention are  
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
XX isolation and characterisation of the DNA and protein sequences of the  
XX invention. The breast and ovarian cancer associated DNA, protein, agonist  
XX or antagonist sequences exhibit cytostatic, immunosuppressive, neurotropic,  
XX neuroprotective, antiviral, antileukemic, hepatotropic, antidiabetic;  
XX antiinflammatory; antitumor; vulnary; anticonvulsant; antibacterial;  
XX antifungal; antiparasitic and cardiant activity. The polynucleotide and  
XX protein sequences are used in the diagnosis of cancer, particularly  
XX breast and ovarian cancer. The nucleic acid sequences, proteins, agonists  
XX and agonists may also be used in the diagnosis, prevention and treatment  
XX of immune disorders e.g. Addison's disease, allergies, autoimmune  
XX haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
XX disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
XX cardiovascular disorders such as myocardial ischaemia; wound healing;  
XX neurological diseases such as cerebral anoxia and epilepsy; and  
XX infectious diseases  
XX  
XX SO Sequence 1336 BP; 318 A; 396 C; 348 G; 270 T; 0 U; 4 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 2.83e-10 Length: 1336  
XX Score: 136.00 Matches: 26  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: Gaps: 0  
XX  
XX US-09-976-740-20 (1-26) x AAF21860 (1-1336)  
XX  
XX QY 1 GluGluGluGluAspAspGluAspGluAspGluGluGluGluGluGluGluGlySer 20  
XX |||||  
XX Db 94 GAAGAGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGCTCT 153  
XX |||||  
XX QY 21 GluValProGluSerAsp 26  
XX |||||  
XX Db 154 GAAGTCCCGAGAGCTGAC 171  
XX |||||  
XX  
XX RESULT 5  
XX AAB26499  
XX ID AAB26499 standard; DNA; 1614 BP.  
XX  
XX AC AAB26499;  
XX XX  
XX DT 12-NOV-2001 (first entry)  
XX

DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.  
 XX Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
 KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
 XX ds.  
 OS Homo sapiens.  
 XX MO200164874-A2.  
 XX PD 07-SEP-2001.  
 XX PF 28-FEB-2001; 2001WO-US006356.  
 XX PR 02-MAR-2000; 2000US-00517849.  
 XX PR 14-JUL-2000; 2000US-00616289.  
 XX PA (BOST-) BOSTON HEART FOUND INC.  
 XX PI Lees AM, Lees RS, Law SW, Arjona AA;  
 XX WPI; 2001-565505/63.  
 XX DR P-PSDB; AAB82806.  
 XX PT New isolated low density lipoprotein binding polypeptide for treating,  
 XX diagnosing and/or identifying therapeutic agents for atherosclerosis.  
 XX PS Claim 7; Fig 7A; 143pp; English.  
 XX  
 CC The present sequence is that of the coding region of the human gene (see  
 CC also AAB82806) encoding novel human low density lipoprotein binding  
 CC protein 2 (LBP-2, see AAB82806). The gene was isolated from a genomic DNA  
 CC library using LBP-2 cDNA as probe. The LBP-2 protein predicted from the  
 CC present sequence differs from that predicted from a cDNA clone (see  
 CC AAB82803) in that it contains an additional 321 amino acids at its N-  
 CC terminus (the cDNA is a 5' truncation). LBP-2 nucleic acids are among  
 CC claimed polynucleotides of the invention that encode novel polypeptides  
 CC capable of binding to native and methylated LDL. Also claimed are  
 CC isolated LBP polypeptides, and biologically active fragments and  
 CC analogues of them as well as expression vectors, cells and methods of  
 CC producing the LBPs. Methods of determining if an animal is at risk for  
 CC atherosclerosis, methods for evaluating an agent for use in treating  
 CC atherosclerosis, and methods for treating a cell having an abnormality in  
 CC structure or metabolism of LBP are claimed. Pharmaceutical compositions  
 CC comprising an LBP polypeptide or nucleic acid, and vaccine compositions,  
 CC are also claimed.  
 CC  
 SQ Sequence 1614 BP; 243 A; 638 C; 564 G; 169 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3,45e-10 Length: 1614  
 Score: 136.00 Matches: 26  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 Gaps: 0  
 US-09-976-740-20 (1-26) x AAB26499 (1-1614)  
 QY 1 GluGluGluGluAspAspGluAspGluAspGluGluAspAspValSerGluGlySer 20  
 Db 985 GAACGAGAAAGAGATGATGTAAGATGAAGATGAAGAGATGATGTCAGAGGCTCT 1044  
 QY 21 GluValProGluSerAsp 26  
 Db 1045 GAAGTGGCCGAGAGTGCAC 1062  
 RESULT 6  
 AAB26495  
 ID AAB26495 standard; DNA; 12425 BP.  
 XX AC AAB26495;  
 XX

DT 12-NOV-2001 (first entry)  
 XX Human low density lipoprotein binding protein 2 (LBP-2) gene.  
 XX Low density lipoprotein binding protein 2; LBP-2; LDL; human;  
 KW atherosclerosis; antiarteriosclerotic; gene therapy; diagnosis; vaccine;  
 XX ds.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 2832..5153  
 XX FT /\*tag= a  
 XX FT /note= "includes introns"  
 XX FT 2832..3785  
 XX FT exon /\*tag= b  
 XX FT 3786..4207  
 XX FT intron /\*tag= c  
 XX FT 4208..4502  
 XX FT exon /\*tag= d  
 XX FT 4503..4593  
 XX FT intron /\*tag= e  
 XX FT 4594..4694  
 XX FT exon /\*tag= f  
 XX FT 4695..4787  
 XX FT intron /\*tag= g  
 XX FT 4788..4899  
 XX FT exon /\*tag= h  
 XX FT 4900..4994  
 XX FT intron /\*tag= i  
 XX FT 4995..5153  
 XX FT exon /\*tag= j  
 XX  
 XX MO200164874-A2.  
 XX PD 07-SEP-2001.  
 XX PF 28-FEB-2001; 2001WO-US006356.  
 XX PR 02-MAR-2000; 2000US-00517849.  
 XX PR 14-JUL-2000; 2000US-00616289.  
 XX PA (BOST-) BOSTON HEART FOUND INC.  
 XX PI Lees AM, Lees RS, Law SW, Arjona AA;  
 XX WPI; 2001-565505/63.  
 XX DR P-PSDB; AAB82806.  
 XX PT New isolated low density lipoprotein binding polypeptide for treating,  
 XX diagnosing and/or identifying therapeutic agents for atherosclerosis.  
 XX PS Example 4; Fig 23; 143pp; English.  
 XX  
 CC The present sequence is that of genomic DNA encoding novel human low  
 CC density lipoprotein binding protein 2 (LBP-2, see AAB82806). The DNA was  
 CC isolated from a human genomic library by screening with LBP-2 cDNA (see  
 CC AAB26494). The open reading frame spans 5 exons. Human LBP-2 nucleic  
 CC acids are among claimed polynucleotides of the invention that encode  
 CC novel polypeptides, termed LBPs, capable of binding to native and  
 CC methylated LDL. Also claimed are isolated LBP polypeptides, and  
 CC biologically active fragments and analogues of them, as well as  
 CC expression vectors, cells and methods of producing the LBPs. Methods of  
 CC determining if an animal is at risk for atherosclerosis, and methods for  
 CC evaluating an agent for use in treating atherosclerosis, and methods for  
 CC treating a cell having an abnormality in structure or metabolism of LBP  
 CC are claimed. Pharmaceutical compositions comprising an LBP polypeptide or  
 CC nucleic acid, and vaccine compositions, are also claimed.  
 CC  
 SQ Sequence 12425 BP; 2563 A; 3702 C; 3566 G; 2594 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2.92e-09 Length: 12425



Score:	104.50	Matches:	20
--------	--------	----------	----





```

XX PF 30-JUL-2001; 2001US-00918995.
XX XX
PR 30-JUL-2001; 2001US-00918995.
XX PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
PS
XX Claim 1; SEQ ID NO 34183; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensic, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030073623
CC
SQ Sequence 415 BP; 97 A; 92 C; 146 G; 80 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0.000577 Length: 415
Score: 88.00 Matches: 14
Percent Similarity: 86.96% Conservative: 6
Best Local Similarity: 60.87% Mismatches: 3
Query Match: 64.71% Indels: 0
DB: 8 Gaps: 0
US-09-976-740-20 (1-26) x ACH46971 (1-415)
QY 1 GUGUGUUGUUAASPAAPGUAAGPGUUGUAASPVALSERGLUGLysR 20
Db 163 GACCAATGAGAAAGCATATGAATGAGACGCACATGATGAGAGAGATCGTAT 222
QY 21 GUUValPro 23
Db 223 GAGGTGGCT 231
RESULT 14
ACH12859
ID ACH12859 standard; cDNA; 421 BP.
XX AC ACH12859;
XX
DT 13-OCT-2003 (first entry)
XX DE Human adult brain cDNA #71.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST
genome mapping; biodiversity; genetic disorder.
```

```
XX Homo sapiens.  
OS  
XX US2003073623-A1.  
PN  
PP 17-APR-2003.  
PD  
PF 30-JUL-2001; 2001US-00918995.  
PR 30-JUL-2001; 2001US-00918995.  
RX  
PA (DSMA/) DRMANAC R T,  
PA (LABA/) LABAT I,  
PA (STAC/) STACHE-CRAIN B,  
PA (DICK/) DICKSON M C,  
PX (JONE/) JONES L W.  
PL Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
DR WP; 2003-615964/58.  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
FT mapping, in the recombinant production of protein, or in generating  
XX antisense DNA or RNA.  
PS Claim 1; SEQ ID NO 71; 44pp; English.  
CC The invention relates to an isolated polynucleotide comprising any one ob  
CC 3843 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antibodies specific for it. The present sequence  
CC is one of the 3843 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPRO at  
CC seqdata.uspro.gov/sequence.html?docID=20030073623  
XX  
SQ Sequence 421 BP; 99 A; 93 C; 147 G; 82 T; 0 U; 0 Other;  
XX Alignment Scores:  
XX Pred. No.: 0.000586 Length: 421  
XX Score: 88.00 Matches: 14  
XX Percent Similarity: 86.96% Conservative: 6  
XX Best Local Similarity: 60.87% Mismatches: 3  
XX Query Match: 64.71% Indels: 0  
XX BB: 8 Gaps: 0
```

```

XX pcENP-B-1 cDNA.
XX
XX Km Centromere protein; antibodies; polypeptide; ss.
XX OS Homo sapiens.
XX JP04334398-A.
XX
XX PD 20-NOV-1992.
XX
XX PF 08-MAY-1991; 91JP-00102517.
XX FR 08-MAY-1991; 91JP-00102517.
XX PA (DAIK ) DAIKIN KOGYO KK.
XX WI: 1993-005542/01.
DR P-PSDB; AAR30641.
XX
XX FT Human centromere antigen polypeptide - for detection of human antibodies
XX and identification of disease.
XX PS
XX PS Disclosure; Fig 4; 15pp; Japanese.
CC
CC Total RNA was extracted from Jurkat cells and mRNA was prep'd. From it, A
CC cDNA library was prep'd. In lambda gIII. A positive clone was isolated and
CC analysed by antibody screening. A mutant coding sequence in which the 3'-
CC terminal sequence was deleted was prepared and used to prepare a
CC polypeptide in which the C-terminal end is deleted. Epitopes of the CEPN-
CC B protein were determined. These peptides can be used to detect anti-
CC human centromere antibodies. The type of diseases of a patient having the
CC antibody can be exactly classified using the polypeptide
XX
SQ Sequence 489 BP; 123 A; 90 C; 186 G; 90 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:          0.000685      Length:         489
Score:              88.00           Matches:         14
Percent Similarity: 86.96%        Conservative:    6
Best Local Similarity: 60.87%     Mismatches:     3
Query Match:       64.71%         Indels:         0
DB:                 2             Gaps:           0

US-09-976-740-20 (1-26) x AAQ34771 (1-489)

QY      1 GIUGIUGIUGIUASPAPSPGLUASPGLUASPGIUGIUASPAPVALSENGUGLYSER 20
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          241 GAAGGATGACGAAGAAGCATGTGAAAGATGAACAAGCAGATGATGATGACGAGAGATGGAT 3000

QY      21 GIUVAIPRO 23
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          301 GAAGTGCTT 309

Search completed: March 12, 2004, 21:08:35
Job time : 47.2118 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 12, 2004, 20:05:17 ; Search time 8.81518 Seconds  
(without alignments)  
1636.805 Million cell updates/sec

Title: US-09-976-740-20  
Perfect score: 136  
Sequence: 1 EEEEDDEDEDEDEDESESESEVPSD 26

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool\_p/US09976740/runat.10032004.094549.19564/app.query.fasta.1.1898  
-DB=Issued\_Patents\_NA -DEXT=fastcap -SUPPLY=emi -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=numan40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09976740@cgn1.1.235 @runat.10032004.094549.19564 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEOUTRY -NEG SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -YGAPOP=6  
-YGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COXB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COXB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COXB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COXB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COXB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	136	100.0	78 4 US-08-979-608A-31	Sequence 31, Appl
2	136	100.0	78 4 US-09-517-849-31	Sequence 31, Appl
3	136	100.0	78 4 US-09-616-289-31	Sequence 31, Appl
4	136	100.0	1208 4 US-08-979-608A-16	Sequence 16, Appl
5	136	100.0	1208 4 US-09-517-849-16	Sequence 16, Appl
6	136	100.0	1208 4 US-09-616-289-16	Sequence 16, Appl
7	136	100.0	1614 4 US-09-616-289-45	Sequence 45, Appl
8	136	100.0	12425 4 US-09-616-289-50	Sequence 50, Appl
9	104.5	76.8	84 4 US-08-979-608A-37	Sequence 37, Appl
10	104.5	76.8	84 4 US-09-517-849-37	Sequence 37, Appl
11	104.5	76.8	84 4 US-09-616-289-37	Sequence 37, Appl
12	104.5	76.8	1362 4 US-08-979-608A-12	Sequence 12, Appl

Result No.	Score	Query Match Length	DB ID	Description
13	104.5	76.8	1362 4 US-09-517-849-12	Sequence 12, Appl
14	104.5	76.8	1362 4 US-09-616-289-12	Sequence 12, Appl
15	104.5	76.8	1422 4 US-08-979-608A-13	Sequence 13, Appl
16	104.5	76.8	1422 4 US-09-517-849-13	Sequence 13, Appl
17	104.5	76.8	1422 4 US-09-616-289-13	Sequence 13, Appl
18	104.5	76.8	1617 4 US-08-979-608A-11	Sequence 11, Appl
19	104.5	76.8	1617 4 US-09-517-849-11	Sequence 11, Appl
20	104.5	76.8	1617 4 US-09-616-289-11	Sequence 11, Appl
21	104.5	76.8	2561 4 US-09-616-289-46	Sequence 46, Appl
22	88	64.7	489 4 US-07-879-685B-3	Sequence 3, Appl
23	82	60.3	45 4 US-08-979-608A-30	Sequence 30, Appl
24	82	60.3	45 4 US-09-517-849-30	Sequence 30, Appl
25	82	60.3	45 4 US-09-616-289-30	Sequence 30, Appl
26	81	59.6	2188 1 US-07-865-662F-10	Sequence 10, Appl
27	81	59.6	2188 3 US-08-374-219B-10	Sequence 10, Appl
28	81	59.6	3489 2 US-08-728-323A-1	Sequence 1, Appl
29	81	59.6	3489 4 US-09-298-568-1	Sequence 1, Appl
30	81	59.6	3489 4 US-09-410-399-1	Sequence 1, Appl
31	81	59.6	32207 2 US-08-770-379-20	Sequence 20, Appl
32	81	59.6	32207 3 US-08-757-669A-20	Sequence 20, Appl
33	81	59.6	32207 4 US-09-230-371A-20	Sequence 20, Appl
34	80	58.8	2518 3 US-09-433-699-3	Sequence 3, Appl
35	79	58.1	2295 1 US-08-375-300-3	Sequence 3, Appl
36	79	58.1	2295 3 US-09-177-431-3	Sequence 3, Appl
37	79	58.1	2295 5 PCT-US95-16930-3	Sequence 3, Appl
38	79	58.1	4080 1 US-08-375-300-1	Sequence 1, Appl
39	79	58.1	4080 3 US-09-177-431-1	Sequence 1, Appl
40	79	58.1	4080 5 PCT-US95-16930-1	Sequence 1, Appl
41	79	58.1	7585 4 US-09-418-710-22	Sequence 22, Appl
42	77	56.6	19056 3 US-09-272-032-8	Sequence 8, Appl
43	77	56.6	19056 4 US-09-443-218-8	Sequence 8, Appl
44	76.5	56.2	4599 1 US-08-431-080-27	Sequence 27, Appl
45	76.5	56.2	4599 2 US-08-938-534-27	Sequence 27, Appl

## ALIGNMENTS

RESULT 1  
US-08-979-608A-31  
; Sequence 31, Application US/08979608A  
; Patent No. 6355451  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Ajona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/979,608A  
FILING DATE: 26-Nov. 6355451-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,547  
FILING DATE: 03-JUN-1997  
APPLICATION NUMBER: US 60/031,990  
FILING DATE: 27-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-08-979-608A-31  
Alignment Scores:  
Pred. No.: 7, 23e-13 Length: 78  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-20 (1-26) x US-08-979-608A-31 (1-78)  
QY 1 GluGlugluGluAspAspGluAspGluAspGluAspAspValSerGluGlySer 20  
DB 1 GAAGAGGAGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 60  
QY 21 GluValProGluSerAsp 26  
DB 61 GAAGTGGCCGAGAGTGAC 78  
RESULT 2  
US-09-517-849-31  
Sequence 31, Application US/09517849  
Patent No. 6605588  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN  
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND  
TREATING ATHEROSCLEROSIS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/517,849  
FILING DATE: 02-Mar-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/979,608  
FILING DATE: 26-NOV-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Louis  
REGISTRATION NUMBER: 35,965  
REFERENCE/DOCKET NUMBER: 10797-003001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:  
LENGTH: 78 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...78  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-517-849-31  
Alignment Scores:  
Pred. No.: 7, 23e-13 Length: 78  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-20 (1-26) x US-09-517-849-31 (1-78)  
QY 1 GluGlugluGluAspAspGluAspGluAspGluAspAspValSerGluGlySer 20  
DB 1 GAAGAGGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 60  
QY 21 GluValProGluSerAsp 26  
DB 61 GAAGTGGCCGAGAGTGAC 78  
RESULT 3  
US-09-616-289-31  
Sequence 31, Application US/09616289  
Patent No. 6632823  
GENERAL INFORMATION:  
APPLICANT: Lees, Ann M.  
Lees, Robert S.  
Law, Simon W.  
Arjona, Anibal A.  
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS  
FILE REFERENCE: 10797-004001  
CURRENT APPLICATION NUMBER: US/09/616,289  
CURRENT FILING DATE: 2000-07-14  
PRIOR APPLICATION NUMBER: US 09/517,849  
PRIOR FILING DATE: 2000-03-02  
PRIOR APPLICATION NUMBER: US 08/979,608  
PRIOR FILING DATE: 1997-11-26  
PRIOR APPLICATION NUMBER: US 60/031,930  
PRIOR FILING DATE: 1996-11-27  
PRIOR APPLICATION NUMBER: US 60/048,547  
PRIOR FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 78  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-616-289-31  
Alignment Scores:  
Pred. No.: 7, 23e-13 Length: 78  
Score: 136.00 Matches: 26  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
DB: 4  
US-09-976-740-20 (1-26) x US-09-616-289-31 (1-78)  
QY 1 GluGlugluGluAspAspGluAspGluAspGluAspAspValSerGluGlySer 20  
DB 1 GAAGAGGAGAGATGATGATGAAGATGAAGATGAAGATGATGTCAGAGGGCTCT 60







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Oy      21 GluValProGluSerAsp 26
Db      4298 GAACTGCCCGAGACTGCAC 4315

RESULT 9
US-08-979-608A-37
Sequence 37, Application US/08979608A
Patent No. 6355451
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
Lees, Robert S.
Law, Simon W.
Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-NOV-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/048,547
FILING DATE: 03-JUN-1997
APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEX: 617/542-8906
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..84
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-979-608A-37

Alignment Scores:
Pred. No.:          3.48e-08      Length:      84
Score:              104.50        Matches:     20
Percent Similarity: 96.30%       Conservative: 6
Best Local Similarity: 74.07%    Mismatches:  0
Query Match:        76.84%       Indels:      1
DB:                  4           Gaps:         1

US-08-976-740-20 (1-26) x US-08-979-608A-37 (1-84)
Oy      1  GluGluGluGluIleuSpaPaSpGluAspGluAspGluGluAspAsp---ValSerGluGly 19
Db      4  GAGGAGGAGGAGGAGGAGGAAGACGACGAGGACGACGACGACGACGTGTGTCCGAGGGC 63
Oy      20  SerGluValProGluSerAsp 26
Db      64  TCGGAGGTGCCCGAGAGCGCAT 84

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RESULT 10
US-09-517-849-37
; Sequence 37, Application US/09517849
; Patent No. 605588
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; Lees, Robert S.
; Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/517,849
; FILING DATE: 02-Mar-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..84
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-517-849-37

Alignment Scores:
Pred. No.: 3,48e-08 Length: 84
Score: 104.50 Matches: 20
Percent Similarity: 96.30% Conservative: 6
Best Local Similarity: 74.07% Mismatches: 0
Query Match: 76.84% Indels: 1
DB: 4 Gaps: 1

US-09-976-740-20 (1-26) x US-09-517-849-37 (1-84)
QY 1 GIUGIUGIUGIUGIUGAPAPAPGIUAEPGIUAEPGIUGIUGIUAASP---Valsergiugiy 19
DB 4 GAGGAGGAGGAGGAGGAGGAGGAGGAGCGACGAGGAGGAGGAGGAGCGTCTGTCCGAGGCG 63
QY 20 SerGIuValProGIuserASP 26
DB 64 TCGGAGGTGCCCGAGGCGCAT 84

RESULT 11
US-09-616-289-37
; Sequence 37, Application US/09616289
; Patent No. 6632823

```

```

: GENERAL INFORMATION:
: APPLICANT: Lees, Ann M.
: APPLICANT: Lees, Robert S.
: APPLICANT: Law, Simon W.
: APPLICANT: Arjona, Anibal A.
: TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
: TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
: TITLE OF INVENTION: ATHEROSCLEROSIS
: FILE REFERENCE: 10797-004001
: CURRENT APPLICATION NUMBER: US/09/616,289
: CURRENT FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: US 09/517,849
: PRIOR FILING DATE: 2000-03-02
: PRIOR APPLICATION NUMBER: US 08/979,608
: PRIOR FILING DATE: 1997-11-26
: PRIOR APPLICATION NUMBER: US 60/031,930
: PRIOR FILING DATE: 1996-11-27
: PRIOR APPLICATION NUMBER: US 60/048,547
: PRIOR FILING DATE: 1997-06-03
: NUMBER OF SEQ ID NOS: 53
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 37
: LENGTH: 84
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-616-289-37

Alignment Scores:
Pred. No.:          3,48e-08      Length:      84
                  104.50        Matches:     20
Percent Similarity: 96.30%       Conservative: 6
Best Local Similarity: 74.07%    Mismatches:   0
Query Match:         76.84%      Indels:       1
DB:                  4           Gaps:          1

US-09-976-740-20 (1-26) x US-09-616-289-37 (1-84)

Cy      1  GLGIUGLIGLUASPAEAPSEGLIUAEPGLIUGLIUASPSP---ValSerGluGly 19
Db      4  GAGAGAGAGAGAGAGAGAGAGAAGCAGACGACGAGACGACGTGTCTCGAGGGC 63

Oy      20 SerGluValProGluSerasp 26
         |||||
Db      64 TCAGAGTGTCCCGAGAGGCAT 84

RESULT 12
US-08-979-608A-12
: Sequence 12, Application US/08979608A
: Patent No. 6355451
: GENERAL INFORMATION:
: APPLICANT: Lees, Ann M.
: APPLICANT: Lees, Robert S.
: APPLICANT: Law, Simon W.
: APPLICANT: Arjona, Anibal A.
: TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
: TITLE OF INVENTION: BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
: TITLE OF INVENTION: TREATING ATHEROSCLEROSIS
: CURRENT APPLICATION NUMBER: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/979,608A
: FILING DATE: 26-No. 6355451-1997

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Prior Application Data:
Application Number: US 60/048,547
Filing Date: 03-JUN-1997
Application Number: US 60/031,930
Filing Date: 27-NOV-1996

Attorney/Agent Information:
Name: Myers, Louis
Registration Number: 35,965
Reference/Docket Number: 10797-002001 (formerly 3983/59818)
Telecommunication Information:
Telephone: 617/542-5070
Telefax: 617/542-8906

Information for SEQ ID NO: 12:
Sequence Characteristics:
Length: 1362 base pairs
Type: nucleic acid
Strandedness: single
Topology: linear

Feature:
Name/Key: Coding Sequence
Location: 1...696
Sequence Description: SEQ ID NO: 12:
US-08-979-608A-12

Alignment Scores:
Pred. No.: 7.09e-07 Length: 1362
Score: 104.50 Matches: 20
Percent Similarity: 96.30% Conservative: 6
Best Local Similarity: 74.07% Mismatches: 0
Query Match: 76.84% Indels: 1
DB: 4 Gaps: 1

US-09-976-740-20 (1-26) x US-08-979-608A-12 (1-1362)

QY      1 GLVLGLGLGLASPAASPGLUASPGLUASPGIUGLUAESP---ValSerGluGly 19
Db      61 GAGGAGGAGGAGGAGGAGGAGACGACGACGACGACGACGCCTGTCCGAGGGC 120

QY      20 SerGluValProGluSerasp 26
Db      121 TCGGAGTGCCCCGAGAGCGAT 141

RESULT 13
US-09-517-849-12
Sequence 12, Application US/09517849
Patent No. 660588
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
               Lees, Robert S.
               Law, Simon W.
               Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
                    BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                    TREATING ATHEROSCLEROSIS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997

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